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More specifically, outlined below is a description as to how an artisan would have utilized the information provided in the subject application, together with technologies and information readily available at the time of filing, to practice the claimed invention.<sup>1</sup> (DDRT 16 is used by way of Example.)

1. The nucleotide sequence of clone DDRT16 is given in Figure 5 of the application (SEQ ID NO:40). (GenBank accession number, AF071356). (See attached Figures 1 and 2.)

2. The nucleotide sequence for DDRT16 can be analyzed using the general nucleotide sequence database and the program BLASTN, which compares nucleotide to nucleotide sequences. (The results of this analysis show that the nucleotide sequence of DDRT16 is identical to itself and that of the *C. elegans* cosmid F35E8.) The results of this analysis are shown in attached Figure 3. This analysis

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<sup>1</sup>All of the programs referenced above are available via the Internet or can be downloaded, free of charge.

For the Examiner's ease of access, the following are provided:

The URL for the Entrez server is: <http://www.ncbi.nlm.nih.gov/Entrez/>

The URL of the GenBank BLAST server is  
<http://www.ncbi.nlm.nih.gov:80/BLAST/>

The URL of the *C. elegans* BLAST server is:  
[http://www.sanger.ac.uk/Projects/C\\_elegans/blast\\_server.shtml](http://www.sanger.ac.uk/Projects/C_elegans/blast_server.shtml)

A description of ACeDb can be found at: <http://www.acedb.org/>

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provides access to the complete genomic sequence of the gene that encoded DDRT16. By entering the accession number for F35E8, 2653095 (see Figure 3), the nucleotide sequence for this cosmid can be obtained.

3. The nucleotide sequence for DDRT16 can be analyzed using the program BLASTN and the *C. elegans* specific genomic nucleotide sequence database. (The results of this analysis show that the nucleotide sequence of DDRT16 is identical to the *C. elegans* cosmid F35E8.) The results of this analysis are shown in attached Figure 4. This analysis provides access to the complete genomic sequence of the gene that encoded DDRT16. By entering the accession number for F35E8, 2653095, the nucleotide sequence for this cosmid can be obtained.

4. The nucleotide sequence for DDRT16 can be analyzed using the *C. elegans* predicted protein amino acid sequence database and the program BLASTX, which compares translated nucleotide sequences to amino acid sequences. (The result of this analysis shows that the protein encoded by the nucleotide sequence of DDRT16 is identical to the predicted *C. elegans* protein F35E8.11.) The results of this analysis are shown in attached Figure 5. This analysis provides access to the complete protein sequence of the DDRT16.

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5. To obtain the complete sequences for the mRNA and protein, the program AceDb can be used. AceDb is a *C. elegans* specific database that contains all of the information related to the *C. elegans* genome. It includes the entire genomic sequence, sequences for the predicted mRNAs, cDNAs and proteins. The data that are presented include introns/exon locations and can be used to identify the regulatory/promoter regions of genes. By searching for F35E8.11 in AceDb, the map of the intron/exon structure, and the cDNA and protein sequences can be obtained (see attached Figures 6-8).

6. By searching for F35E8 in AceDb, the entire nucleotide sequence for this cosmid can be obtained. By knowing the start codon for F35E8.11 and the location of the adjacent gene, the regulatory region/promoter for this gene can be predicted.

Summarizing, given the accession number for the sequence data provided in the application, any person with minimal molecular biology experience can readily obtain the complete gene, mRNA and protein sequences, using freely available, user-friendly programs and data analysis software available via the Internet. Accordingly, it should be clear that Applicants had full possession of the claimed invention at the time of filing and further that

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the disclosure provided is enabling. Reconsideration is thus requested.

This application is submitted to be in condition for allowance and a Notice to that effect is requested.

Respectfully submitted,

**NIXON & VANDERHYE, P.C.**



By

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Reg. No. 32,955

MJW:tat

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Facsimile: (703) 816-4100

PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

Search Nucleotide ☒ For AF071356

1: AF071356

PubMed, Taxonomy

AF071356 mRNA from cadmium-responsive gene *Caenorhabditis elegans*  
cDNA clone DDRT16, mRNA sequence  
[gi|3265101|gb|AF071356.1|AF071356\[3265101\]](#)

Revised: March 12, 2001.

[Disclaimer](#) | [Write to the Help Desk](#)  
[NCBI](#) | [NLM](#) | [NIH](#)

## Figure 2



Nucleotide

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search Nucleotide		Limits		Index		History	
Display		Default View		as HTML		Save	
Go		Clear		Clipboard		Add to Clipboard	

1: AF071356 **AF071356 mRNA from cadmium-responsive gene  
Caenorhabditis elegans cDNA clone DDRT16, mRNA  
sequence**

PubMed, Taxonomy, LinkOut

## IDENTIFIERS

dbEST Id: 1777139  
EST name: AF071356  
GenBank Acc: AF071356  
GenBank gi: 3265101

## CLONE INFO

Clone Id: DDRT16  
DNA type: cDNA

## PRIMERS

PolyA Tail: Unknown

## SEQUENCE

TTTTTTTTTTTTGGGAGGAAATCACGGCGGGCGGATGCAACAGTCTTCTCTCAATTGGCA  
ACTGTCATTATCCATTCCGCAATCACATTTTCGGATGTTCTCGAAAAGGACTTCCCAAAG  
TTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTACCCAAAGGACTTTACTATGTGA  
ATTAAATTGTCAAACCTAGTAGTCAGATCAATAAAATTCTACGTGGCAAAAAAAAAAAAA

Entry Created: Jun 30 1998  
Last Updated: Nov 25 1998

## LIBRARY

Lib Name: mRNA from cadmium-responsive gene  
Organism: Caenorhabditis elegans  
Strain: N2  
Tissue type: whole animal  
Develop. stage: mixed population

## SUBMITTER

Name: Jonathan H. Freedman  
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E-mail: jonf@duke.edu

## CITATIONS

Medline UID: 99041962  
Title: Cadmium-regulated genes from the nematode *Caenorhabditis elegans*. Identification and cloning of new cadmium-responsive genes by differential display  
Authors: Liao, V.H.-C., Freedman, J.H.  
Citation: J. Biol. Chem. 273 (48): 31962-70 1998

## MAP DATA

# Figure 3



## results of BLAST

BLASTN 2.1.3 [Apr-11-2001]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 990026953-3242-12725

Query= gi|3265101|gb|AF071356.1|AF071356 AF071356 mRNA from cadmium-responsive gene Caenorhabditis elegans cDNA clone DDRT16, mRNA sequence (238 letters)

Database: nt

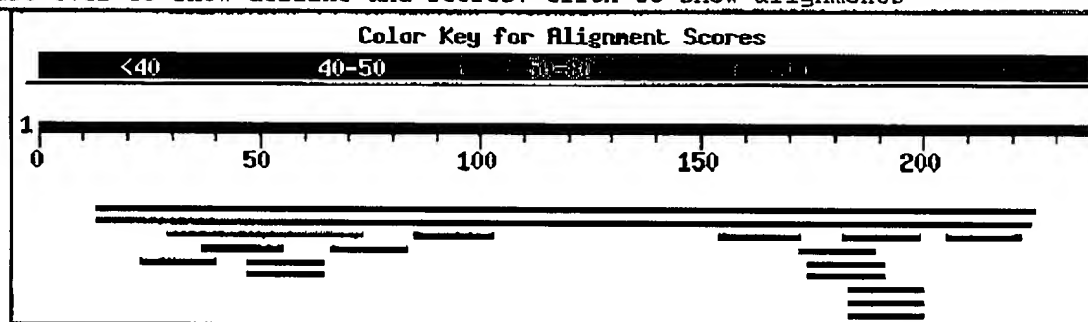
861,799 sequences; 3,247,139,289 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports

### Distribution of 19 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Sequences producing significant alignments:					Score	E
					(bits)	Value
gi 11120428 gb AF301606.1 AF301606	Caenorhabditis elegans c...	422	e-116			
gi 2653095 emb Z81529.1 CEF35E8	Caenorhabditis elegans cosm...	381	e-103			
gi 1418539 emb Z75543.1 CEK01D12	Caenorhabditis elegans cos...	50	6e-04			
gi 12620418 gb AF322012.1 AF322012S1	Bradyrhizobium japonic...	38	2.3			
gi 4982441 gb AE001823.1 AE001823	Thermotoga maritima secti...	38	2.3			
gi 1627880 emb Z81074.1 CEF32B6	Caenorhabditis elegans cosm...	38	2.3			
gi 12583776 gb AC010585.6 AC010585	Homo sapiens chromosome ...	36	9.0			
gi 10727249 gb AE003475.2 AE003475	Drosophila melanogaster ...	36	9.0			
gi 7301915 gb AE003773.1 AE003773	Drosophila melanogaster g...	36	9.0			
gi 10043285 gb AC003046.3 AC003046	Homo sapiens Xp22 PACs R...	36	9.0			

gi 6598428 gb AC004665.2 AC004665	Arabidopsis thaliana chro...	36	9.0
gi 6409187 gb AF145126.1 DRMFER2	Drosophila melanogaster fe...	36	9.0
gi 3212170 gb AF001905.1 AF001905	Homo sapiens cosmid E079...	36	9.0
gi 11229166 emb AL357892.13 AL357892	Human DNA sequence fro...	36	9.0
gi 5531462 emb AL096851.1 SPBC1105	S.pombe chromosome II co...	36	9.0
gi 1301745 emb Z72519.1 HSJ13817A	Human DNA sequence from c...	36	9.0
gi 7768698 dbj AP001686.1 AP001686	Homo sapiens genomic DNA...	36	9.0
gi 7077191 dbj AP001255.1 AP001255	Homo sapiens genomic DNA...	36	9.0

## Alignments

>gi|11120428|gb|AF301606.1|AF301606 Caenorhabditis elegans cadmium-inducible lysosomal ;  
(cdr-1) mRNA, complete cds  
Length = 907

Score = 422 bits (213), Expect = e-116  
Identities = 213/213 (100%)  
Strand = Plus / Plus

Query: 14 gggaggaaatcacggcgcgcgatgcaacagttcttctctcaattggcaactgtctattatc 73  
|||||  
Sbjct: 683 gggaggaaatcacggcgcgcgatgcaacagttcttctctcaattggcaactgtctattatc 742

Query: 74 cattccgcaatcacatttcggatgttctcgaaaaggacttcccaaagttattggagtact 133  
|||||  
Sbjct: 743 cattccgcaatcacatttcggatgttctcgaaaaggacttcccaaagttattggagtact 802

Query: 134 gtgaaagagttcgtcatgaagtttaccxaaaggactttactatgtgaattaaattgtcaa 193  
|||||  
Sbjct: 803 gtgaaagagttcgtcatgaagtttaccxaaaggactttactatgtgaattaaattgtcaa 862

Query: 194 actagtagtcagatcaataaaaattctacgtggc 226  
|||||  
Sbjct: 863 actagtagtcagatcaataaaaattctacgtggc 895

>gi|2653095|emb|Z81529.1|CEF35E8 Caenorhabditis elegans cosmid F35E8, complete sequence  
Length = 23602

Score = 381 bits (192), Expect = e-103  
Identities = 195/196 (99%)  
Strand = Plus / Plus

Query: 30 ggcggatgcaacagttcttctctcaattggcaactgtctattatccattccgcaatcacat 89  
|||||  
Sbjct: 18625 ggcggatgcaacagttcttctctcaattggcaactgtctattatccattccgcaatcacat 18684

Query: 90 ttcggatgttctcgaaaaggacttcccaaagttattggagtactgtgaaagagttcgtca 149  
|||||  
Sbjct: 18685 ttcggatgttctcgaaaaggacttcccaaagttattggagtactgtgaaagagttcgtca 18744

Query: 150 tgaagtttaccxaaaggactttactatgtgaattaaattgtcaaactagtagtcagatca 209  
|||||  
Sbjct: 18745 tgaagtttaccxaaaggactttactatgtgaattaaattgtcaaactagtagtcagatca 18804

Query: 210 ataaaaattctacgtgg 225  
|||||



gi 6598428 gb AC004665.2 AC004665	Arabidopsis thaliana chro...	36	9.0
gi 6409187 gb AF145126.1 DRMFER2	Drosophila melanogaster fe...	36	9.0
gi 3212170 gb AF001905.1 AF001905	Homo sapiens cosmids E079...	36	9.0
gi 11229166 emb AL357892.13 AL357892	Human DNA sequence fro...	36	9.0
gi 5531462 emb AL096851.1 SPBC1105	S.pombe chromosome II co...	36	9.0
gi 1301745 emb Z72519.1 HSJ13817A	Human DNA sequence from c...	36	9.0
gi 7768698 dbj AF001686.1 AF001686	Homo sapiens genomic DNA...	36	9.0
gi 7077191 dbj AF001255.1 AF001255	Homo sapiens genomic DNA...	36	9.0

## Alignments

>gi|11120428|gb|AF301606.1|AF301606 Caenorhabditis elegans cadmium-inducible lysosomal  
(cdr-1) mRNA, complete cds  
Length = 907

Score = 422 bits (213), Expect = e-116  
Identities = 213/213 (100%)  
Strand = Plus / Plus

Query: 14 gggaggaaatcacggcgggcgatgcaacagtccttctctcaattggcaactgtctattatc 73  
|||||  
Sbjct: 683 gggaggaaatcacggcgggcgatgcaacagtccttctctcaattggcaactgtctattatc 742

Query: 74 cattccgcaatcacatttcggatgttctcgaaaaggacttcccaaagttattggagtact 133  
|||||  
Sbjct: 743 cattccgcaatcacatttcggatgttctcgaaaaggacttcccaaagttattggagtact 802

Query: 134 gtgaaagagttcgtcatgaagtttaccctaaaggactttactatgtgaattaaattgtcaa 193  
|||||  
Sbjct: 803 gtgaaagagttcgtcatgaagtttaccctaaaggactttactatgtgaattaaattgtcaa 862

Query: 194 actagtagtcagatcaataaaaattctacgtggc 226  
|||||  
Sbjct: 863 actagtagtcagatcaataaaaattctacgtggc 895

>gi|2653095|emb|Z81529.1|CEB35E8 Caenorhabditis elegans cosmid F35E8, complete sequence  
Length = 23602

Score = 381 bits (192), Expect = e-103  
Identities = 195/196 (99%)  
Strand = Plus / Plus

Query: 30 ggcggatgcaacagtccttctctcaattggcaactgtctattatccattccgcaatcacat 89  
|||||  
Sbjct: 18625 ggcggatgcaacagtccttctctcaattggcaactgtctattatccattccgcaatcacat 18684

Query: 90 ttcggatgttctcgaaaaggacttcccaaagttattggagtactgtgaaagagttcgtca 149  
|||||  
Sbjct: 18685 ttcggatgttctcgaaaaggacttcccaaagttattggagtactgtgaaagagttcgtca 18744

Query: 150 tgaagtttaccctaaaggactttactatgtgaattaaattgtcaaactagtagtcagatca 209  
|||||  
Sbjct: 18745 tgaagtttaccctaaaggactttactatgtgaattaaattgtcaaactagtagtcagatca 18804

Query: 210 ataaaattctacgtgg 225  
|||||

Sbjct: 18805 ataaaattttacgtgg 18820

Score = 36.2 bits (18), Expect = 9.0  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 14 gggaggaaatcacggcgg 31

|||||

Sbjct: 18556 gggaggaaatcacggcgg 18573

>[gi|1418539|emb|Z75543.1|CEK01D12](#) *Caenorhabditis elegans* cosmid K01D12, complete sequence  
Length = 36974

Score = 50.1 bits (25), Expect = 6e-04  
Identities = 40/45 (88%)  
Strand = Plus / Minus

Query: 30 ggcggatgcaacagttcttctcaattggcaactgtctattatcc 74

|||||

Sbjct: 31282 ggcggatgcaacagttgttggtcaattggcaactgtatattatcc 31238

>[gi|12620418|gb|AF322012.1|AF322012S1](#) *Bradyrhizobium japonicum* symbiotic gene region, partial  
Length = 180000

Score = 38.2 bits (19), Expect = 2.3  
Identities = 19/19 (100%)  
Strand = Plus / Minus

Query: 155 tttacccaaaggactttac 173

|||||

Sbjct: 57778 tttacccaaaggactttac 57760

>[gi|4982441|gb|AE001823.1|AE001823](#) *Thermotoga maritima* section 135 of 136 of the complete genome  
Length = 12762

Score = 38.2 bits (19), Expect = 2.3  
Identities = 19/19 (100%)  
Strand = Plus / Minus

Query: 86 acatttcggatgttctcga 104

|||||

Sbjct: 5927 acatttcggatgttctcga 5909

>[gi|1627880|emb|Z81074.1|CEF32B6](#) *Caenorhabditis elegans* cosmid F32B6, complete sequence  
Length = 27394

Score = 38.2 bits (19), Expect = 2.3  
Identities = 19/19 (100%)  
Strand = Plus / Minus

Query: 38 caacagtcttctctcaatt 56

|||||

Sbjct: 21939 caacagtcttctctcaatt 21921

>[gi|12583776|gb|AC010585.6|AC010585](#) *Homo sapiens* chromosome 5 clone CTC-315024, complete sequence  
Length = 174882

Score = 36.2 bits (18), Expect = 9.0  
Identities = 18/18 (100%)

Strand - Plus / Minus

Query: 173 ctatgtgaattaaattgt 190

|||||

Sbjct: 53097 ctatgtgaattaaattgt 53080

>gi|10727249|gb|AE003475.2|AE003475 *Drosophila melanogaster* genomic scaffold 14200001336  
complete sequence  
Length = 300829

Score = 36.2 bits (18), Expect = 9.0

Identities = 18/18 (100%)

Strand = Plus / Minus

Query: 24 cacggcgcgcgatgcaac 41

|||||

Sbjct: 163288 cacggcgcgcgatgcaac 163271

>gi|7301915|gb|AE003773.1|AE003773 *Drosophila melanogaster* genomic scaffold 14200001336  
105, complete sequence  
Length = 226905

Score = 36.2 bits (18), Expect = 9.0

Identities = 18/18 (100%)

Strand = Plus / Minus

Query: 175 atgtgaattaaattgtca 192

|||||

Sbjct: 183441 atgtgaattaaattgtca 183424

>gi|10043285|gb|AC003046.3|AC003046 *Homo sapiens* Xp22 PACs RPC11-263P4 and RPC11-164K3 c  
Length = 166758

Score = 36.2 bits (18), Expect = 9.0

Identities = 18/18 (100%)

Strand = Plus / Minus

Query: 206 atcaataaaattctacgt 223

|||||

Sbjct: 104081 atcaataaaattctacgt 104064

>gi|6598428|gb|AC004665.2|AC004665 *Arabidopsis thaliana* chromosome II section 244 of 25:  
sequence. Sequence from clones F17K2, F4I18  
Length = 89794

Score = 36.2 bits (18), Expect = 9.0

Identities = 18/18 (100%)

Strand = Plus / Plus

Query: 183 taaattgtcaaactagta 200

|||||

Sbjct: 27994 taaattgtcaaactagta 28011

>gi|6409187|gb|AF145126.1|DRMFER2 *Drosophila melanogaster* ferritin gene cluster  
Length = 3066

Score = 36.2 bits (18), Expect = 9.0

Identities = 18/18 (100%)

Strand = Plus / Minus

Query: 175 atgtgaattaaattgtca 192

|||||

Sbjct: 719 atgtgaattaaattgtca 702

>[gi|3212170|gb|AF001905.1|AF001905](#) Homo sapiens cosmids E079, B0920 and A8 from Xq25 X-1 lymphoproliferative disease gene candidate region, complete sequence  
Length = 197620

Score = 36.2 bits (18), Expect = 9.0  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 18 ctctcaattggcaactgt 65

|||||

Sbjct: 94392 ctctcaattggcaactgt 94375

>[gi|11229166|emb|AL357892.13|AL357892](#) Human DNA sequence from clone RP11-707H15 on chromosome 11p15.5  
sequence [Homo sapiens]  
Length = 189876

Score = 36.2 bits (18), Expect = 9.0  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 184 aaattgtcaaactagtag 201

|||||

Sbjct: 148220 aaattgtcaaactagtag 148237

>[gi|5531462|emb|AL096851.1|SPBC1105](#) S.pombe chromosome II cosmid c1105  
Length = 34982

Score = 36.2 bits (18), Expect = 9.0  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 67 tattatccattccgcaat 84

|||||

Sbjct: 16858 tattatccattccgcaat 16875

>[gi|1301745|emb|Z72519.1|HSJ13817A](#) Human DNA sequence from cosmid J138017, between markers DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element  
Length = 125787

Score = 36.2 bits (18), Expect = 9.0  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 48 ctctcaattggcaactgt 65

|||||

Sbjct: 94392 ctctcaattggcaactgt 94375

>[gi|7768698|dbj|AP001686.1|AP001686](#) Homo sapiens genomic DNA, chromosome 21q, section 30  
Length = 340000

Score = 36.2 bits (18), Expect = 9.0  
Identities = 18/18 (100%)

Strand = Plus / Minus

Query: 184 aaattgtcaaactagtag 201  
|||||||  
Sbjct: 280556 aaattgtcaaactagtag 280539

>gi|7077191|dbj|AP001255.1|AP001255 Homo sapiens genomic DNA, chromosome 21q21.1-q21.2,  
LL56-APP region, complete sequence  
Length = 83921

Score = 36.2 bits (18), Expect = 9.0  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 184 aaattgtcaaactagtag 201  
|||||||  
Sbjct: 50434 aaattgtcaaactagtag 50417

Database: nt  
Posted date: May 11, 2001 4:10 AM  
Number of letters in database: -1,072,656,299  
Number of sequences in database: 858,416

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3  
Gap Penalties: Existence: 5, Extension: 2  
Number of Hits to DB: 355216  
Number of Sequences: 858416  
Number of extensions: 355216  
Number of successful extensions: 26098  
Number of sequences better than 10.0: 18  
length of query: 238  
length of database: 3,222,310,993  
effective HSP length: 19  
effective length of query: 219  
effective length of database: 3,206,001,089  
effective search space: 702114238491  
effective search space used: 702114238491  
T: 0  
A: 30  
X1: 6 (11.9 bits)  
X2: 15 (29.7 bits)  
S1: 12 (24.3 bits)  
S2: 18 (36.2 bits)

## Figure 4



Intranet | Sanger Centre | Acedb | Acebrowser | Ensembl | Trace Server | Library  
 Info | Database Searches | HGP | Projects | Software | Teams | Search



Data Release Policy | Conditions of Use

## Blast Server Results

powered by  
**COMPAQ NonStop**

Low complexity filtering disabled  
 Repeatmasker disabled

BLASTN 2.0a13MP-WashU [10-Jun-1997] [Build 23:08:16 Jun 10 1997]

Reference: Gish, Warren (1994-1997). unpublished.

Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find nearly identical sequences rapidly. To identify weak similarities encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= gi  
 (238 letters)

Database: wormpub/allcmid  
 3692 sequences; 104,258,147 total letters.

Searching....10.....20.....30.....40.....50.....60.....70.....80.....90.....100% done

		Smallest Sum		
		High Score	Probability P(N)	N
Sequences producing High-scoring Segment Pairs:				
F35E8	ACC=Z81529	<u>971</u>	8.1e-38	1
K01D12	ACC=Z75543	<u>451</u>	2.6e-14	1
C54D10	ACC=Z75531	<u>451</u>	2.6e-14	1
C07A4	ACC=Z78536	<u>163</u>	0.24	1
Y71G12B	ACC=AC025726	<u>143</u>	0.39	2
Y49F6A	ACC=AC024800	<u>153</u>	0.53	1
F54B3	ACC=Z48583	<u>152</u>	0.57	1
C03A7	ACC=AF016451	<u>152</u>	0.57	1
ZK287	ACC=Z70757	<u>149</u>	0.69	1
Y22D7AL	ACC=AC084153	<u>147</u>	0.76	1
Y11D7A	ACC=AL032632	<u>146</u>	0.80	1
C46E10	ACC=AF039710	<u>145</u>	0.83	1
F23H11	ACC=AF003389	<u>144</u>	0.86	1
T24C4	ACC=AF100306	<u>144</u>	0.86	1
Y53H1A	ACC=AL132864	<u>143</u>	0.89	1
T07C12	ACC=Z73976	<u>143</u>	0.89	1
B0285	ACC=Z34533	<u>143</u>	0.89	1
F10G2	ACC=U64836	<u>142</u>	0.91	1
Y48G1A	ACC=AC024792	<u>142</u>	0.91	1
F56G4	ACC=Z81552	<u>141</u>	0.93	1
W03B1	ACC=U58753	<u>141</u>	0.93	1
Y48A6B	ACC=AL023844	<u>141</u>	0.93	1

T24C12	ACC=U41037	<u>140</u>	0.95	1
F21D5	ACC=Z54271	<u>140</u>	0.95	1
Y54B5A	ACC=AL032643	<u>140</u>	0.95	1
Y47D3A	ACC=AL117202	<u>140</u>	0.95	1
ZK675	ACC=Z46812	<u>138</u>	0.97	1
ZK1025	ACC=AL022288	<u>138</u>	0.97	1
D1065	ACC=AF016414	<u>137</u>	0.98	1
LLC1	ACC=Z82277	<u>137</u>	0.98	1
Y71F9AR	ACC=AC024853	<u>137</u>	0.98	1
Y53F4B	ACC=AL132949	<u>137</u>	0.98	1
R10E11	ACC=Z29095	<u>136</u>	0.9999	1
F43C1	ACC=Z46937	<u>136</u>	0.9999	1
C44H4	ACC=Z79598	<u>136</u>	0.9999	1

>F35E8 [Full Sequence] [AceBrowser] ACC=Z81529  
Length = 23,602

## Plus Strand HSPs:

Score = 971 (145.7 bits), Expect = 8.1e-38, P = 8.1e-38

Identities = 195/196 (99%), Positives = 195/196 (99%), Strand = Plus / Plus

Query: 30 GCGCGATGCAACAGTCTTCTCTCAATTGGCAACTGTCTATTATCCATTCCGCAATCACAT 89  
|||||  
Sbjct: 18625 GCGCGATGCAACAGTCTTCTCTCAATTGGCAACTGTCTATTATCCATTCCGCAATCACAT 18684

Query: 90 TTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCA 149  
|||||  
Sbjct: 18685 TTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCA 18744

Query: 150 TGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAAGTAGTAGTCAGATCA 209  
|||||  
Sbjct: 18745 TGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAAGTAGTAGTCAGATCA 18804

Query: 210 ATAAATTTCTACGTGG 225  
|||||  
Sbjct: 18805 ATAAATTTTACGTGG 18820

Score = 145 (21.8 bits), Expect = 1.8, P = 0.83

Identities = 47/65 (72%), Positives = 47/65 (72%), Strand = Plus / Plus

Query: 4 TTTT TTTT TTTT GGGAGGAAATCACGGCGGGATGCAACAGTCTTCTCTCAATTGGCAACT 63  
TTT TTTT GGGAGGAAATCACGGCGG AT CA CAGTCT T AATTG A CT  
Sbjct: 18546 TTTCTTTTTCGGGAGGAAATCACGGCGGTAAATACA-CAGTCTAATAA-AATTGT-ATCT 18602

Query: 64 GTCTA 68  
G C A  
Sbjct: 18603 GGCAA 18607

>K01D12 [Full Sequence] [AceBrowser] ACC=Z75543  
Length = 36,974

## Minus Strand HSPs:

Score = 451 (67.7 bits), Expect = 2.6e-14, P = 2.6e-14

Identities = 157/231 (67%), Positives = 157/231 (67%), Strand = Minus / Plus

Query: 235 TTTT TTTT TTTT GCCACGTAGAAATTTTATTGATCTGACTACTAGTTTGACAATTTAAT-TCAC 177  
TTTTT TG CACG A A TTTATT TC A A T A AAT A T TCA

Sbjct: 34627 TTTTTCAGTGTACAG-ATTAGTTTATT--TCAAAAAAGTTACCGCATAATACATTCTCAA 34683

Query: 176 ATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTTCACAGTACTCCAATAACTTT 117  
ATAGTAAA TC TTGG TAAA TTC T CG A TCTTTCACAGTACT A A CTTT

Sbjct: 34684 ATAGTAAAATCATTGGATAAATTTCTTTTCGGATTCTTTTCACAGTACTGTAGAATCTTT 34743

Query: 116 GGGAAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAATGGATAATAGACAGTTGCC 57  
GGGAA TC TTTTC AGAACA GA ATGTGA TG AATGGATAATA ACA TGCC

Sbjct: 34744 GGGAAATCATTTCAGAAGACAGTAGAGATGTGAGTGTAATGGATAATAACAACACTGCC 34803

Query: 56 AATTGAGAGAAGACTGTTGCATCCGCCGCCGTGATTTCTCTC-CCAAAAA 5  
AA TG AA AC GT GCATC C G G AT T TC CAAA AAA A

Sbjct: 34804 AACTGGCTAAAAACCGTCGCATCAACTGGAGCAATGTGGTCTCCAAATAATA 34856

Score = 421 (63.2 bits), Expect = 6.0e-13, P = 6.0e-13

Identities = 123/166 (74%), Positives = 123/166 (74%), Strand = Minus / Plus

Query: 195 GTTTGACAATTTAATTCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTC 136  
GTTT A AA T AATTCA AT GTAAA TC TT GG TA A TTC T CG ACTCTTTC

Sbjct: 31118 GTTTCAAAAAT-AATTCAAATTGTAAATCGTTAGGATAGATTTCTTTGCGTACTCTTTC 31176

Query: 135 ACAGTACTCCAATAACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAA 76  
A TA TC A A CTT GGGAA TC TT TC AGAACATC G A TGA CG AA

Sbjct: 31177 CAAATATTCAAGCACCTTGGGGAAATCTTTGTCAAGAACATCGGTGAGATGAGAACG-AA 31235

Query: 75 T-GGATAATAGACAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCC 30  
T GGATAATA ACAGTTGCCAATTGA AA ACTGTTGCATCCGCC

Sbjct: 31236 TAGGATAATATACAGTTGCCAATTGACCAAACACTGTTGCATCCGCC 31282

>C54D10 [Full Sequence] [AceBrowser] ACC=Z75531  
Length = 40,450

Minus Strand HSPs:

Score = 451 (67.7 bits), Expect = 2.6e-14, P = 2.6e-14

Identities = 157/231 (67%), Positives = 157/231 (67%), Strand = Minus / Plus

Query: 235 TTTTTTTTTGCCACGTAGAATTTTATTGATCTGACTACTAGTTTGACAATTTAAT-TCAC 177  
TTTT TG CACG A A TTTATT TC A A T A AAT A T TCA

Sbjct: 1867 TTTTGTAGTGTACAG-ATTAGTTTATT--TCAAAAAAGTTACCGCATAATACATTCTCAA 1923

Query: 176 ATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTTCACAGTACTCCAATAACTTT 117  
ATAGTAAA TC TTGG TAAA TTC T CG A TCTTTCACAGTACT A A CTTT

Sbjct: 1924 ATAGTAAAATCATTGGATAAATTTCTTTTCGGATTCTTTTCACAGTACTGTAGAATCTTT 1983

Query: 116 GGGAAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAATGGATAATAGACAGTTGCC 57  
GGGAA TC TTTTC AGAACA GA ATGTGA TG AATGGATAATA ACA TGCC

Sbjct: 1984 GGGAAATCATTTCAGAAGACAGTAGAGATGTGAGTGTAATGGATAATAACAACACTGCC 2043

Query: 56 AATTGAGAGAAGACTGTTGCATCCGCCGCCGTGATTTCTCTC-CCAAAAA 5  
AA TG AA AC GT GCATC C G G AT T TC CAAA AAA A

Sbjct: 2044 AACTGGCTAAAAACCGTCGCATCAACTGGAGCAATGTGGTCTCCAAATAATA 2096

Score = 352 (52.8 bits), Expect = 7.8e-10, P = 7.8e-10

Identities = 122/178 (68%), Positives = 122/178 (68%), Strand = Minus / Plus

Query: 183 AATTCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTTCACAGTACTCCAA 124  
AATT A AT GTAAA TC TTGG TA A TTC TGACGAACTC TTCACA TA TCCA

Sbjct: 5615 AATTAA-ATTGTAAAATCATTGGATATATTTCTGACGAACTCGTTTCAATATTCCAG 5673



Query: 123 TAACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATG-TGATTGCGGAATGGATAATAGA 65  
 A TTTGGGAA TC TTTTC AG CATC AT TG CGGAATGGATAA A  
 Sbjct: 5674 AATTTTTGGGAATCATTTTCAAGGGCATCGTTGATACTGCAC-CGGAATGGATAAATCA 5732

Query: 64 CAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCCGCCGTGATTTCCTCCCAAAAAA 6  
 C G GC A TTGA AA AC G TGCATC GCC G ATTT T A AAAAAA  
 Sbjct: 5733 CCGACGCAATTTGACCAAATACAGCTGCATCTGCCT--GAAATTTTATGAGATAAAAAA 5789

Score = 296 (44.4 bits), Expect = 2.7e-07, P = 2.7e-07  
 Identities = 110/162 (67%), Positives = 110/162 (67%), Strand = Minus / Plus

Query: 191 GACAATTTAATTCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAG 132  
 GA AA TTA TTCA A A AAA TC TTTGG TAAA TC T CGAAC C TC CA  
 Sbjct: 7285 GAAAAGTTA-TTCA-ACA--AAA-TCATTTGGATAAATCTCTTTGCGAACACGCTCGCAA 7339

Query: 131 TACTCCAATAACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAATGGA 72  
 TA TCCA A CT GG AA TC TTTTC AGAA ATC AAT T GCGGAATGGA  
 Sbjct: 7340 TATTCAGAAAGCTGAGGAAAATCATTTTCCAGAATATCGTTAATTTTGCAGCGGAATGGA 7399

Query: 71 TAA-TAGACAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCC 30  
 TAA TA AC GT GC A TTG AA ACTG TGC TC GCC  
 Sbjct: 7400 TAAATA-ACTGTGGCGAGTTGTCCAAAACTGCTGCGTCTGCC 7441

>C07A4 [Full Sequence] [AceBrowser] ACC=Z78536  
 Length = 16,878

Minus Strand HSPs:

Score = 163 (24.5 bits), Expect = 0.27, P = 0.24  
 Identities = 135/220 (61%), Positives = 135/220 (61%), Strand = Minus / Plus

Query: 237 TTTT TTTT TTTT GCCACGTAGAATTT-TATTGATCTGACTACTAGTTTGACAATTTAAT-T 180  
 T TT TTT T G C C A AAT T TATT TC ACTACTAGTTTG AA AAT T  
 Sbjct: 3342 TATTGTTTGTCTCTCAGAAAATATGTATTTTCC-ACTACTAGTTTGCAAAGAAAATAT 3400

Query: 179 CACATAGTA-AAGTCCTTTGGGTAAACTTCATGACGAACT-CTTTCACAGTACTCCAATA 122  
 A TAGTA AA T TTTG A ACTTCAT A A CT C TTCA A T CT TA  
 Sbjct: 3401 GATTTAGTATAAATT-TTTGAC-ATACCTCATAAAAATCTGCATTCA-ATTCCTGAGGTA 3457

Query: 121 A-CTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCC-G-AATGGATAATAGA 65  
 C TT G TTT G AA GAAA T ATT G G AA GATAATA  
 Sbjct: 3458 TTCCTTTATTCGGATGTTT-GT-AATTGGTGAAAGTTTATTTTGTGTAAAAGATAATA-- 3513

Query: 64 CAGTTGCCAATTGAGAG--AAGACTGTTCATCCGCCGC-CGTGATTTC 18  
 C GT G AT GAGA AA AC GT G AT GC GC C TGATTTC  
 Sbjct: 3514 C-GT-GAAGAT-GAGAATAAAAACAGTAGGATA-GCGGCTCCTGATTTTC 3559

>Y71G12B [Full Sequence] [AceBrowser] ACC=AC025726  
 Length = 191,954

Plus Strand HSPs:

Score = 143 (21.5 bits), Expect = 0.50, Sum P(2) = 0.39  
 Identities = 117/199 (58%), Positives = 117/199 (58%), Strand = Plus / Plus

Query: 43 GTCTTCTCTCAATTGGCAA-CTGTCTATTATCCATTCCGCAATCACATT--TC-GGATGT 98

GT TTCT T AA T CAA CTG ATT TCCATT AAT A A T GG TG  
 Sbjct: 125097 GTTTTCTGTGAAATTTCAAGCTGAA-ATT-TCCATTTTGAATAAAAAAATGTGGCTGG 125154

Query: 99 -TCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGA-GTTCGTCA-TGAAGT 155  
 T T AAAA AC AAA T ATT ACTG AAA GT TC TGAA T

Sbjct: 125155 ATTTAAAAAAAACCATTAAATTTGATTTTAACTGAAAAATCCGTATTTCTCTGAAAT 125214

Query: 156 TT-ACCCAAAGGACTTTACTATGTGAA-TTAAATTGTCAAAGTAGTACAGATCAATAA 213  
 TT A CAAA A T A T T GAA TAAA T AC A A TCA AT AA

Sbjct: 125215 TTCAGGCAAAAAATGTCATT-TCCGAAATTAAAAATTGCGACAAA-A-TCAAATAAAATT 125271

Query: 214 AATTCTACGTGGCAAAAAAAAAAAAA 238  
 AT C A T GCAAAAAAAAAAAAA

Sbjct: 125272 GAT-CAAAATTTGCAAAAAAAAAAAAA 125295

Score = 107 (16.1 bits), Expect = 0.50, Sum P(2) = 0.39

Identities = 33/46 (71%), Positives = 33/46 (71%), Strand = Plus / Plus

Query: 1 TTTTTTTTTTTTTGGGAGGAAATCACGGCGCGGATG-CAACAGTC 45  
 TTTTTTTTTTTTG GA A TCAC CG CG AT CAA A TC

Sbjct: 56244 TTTTTTTTTTTTGAGAAATATTCACAACGTCGCATTACAAAATTC 56289

>Y49F6A [Full Sequence] [AceBrowser] ACC=AC024800  
 Length = 24,330

Plus Strand HSPs:

Score = 153 (23.0 bits), Expect = 0.77, P = 0.53

Identities = 67/99 (67%), Positives = 67/99 (67%), Strand = Plus / Plus

Query: 140 GAGT-TCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAA-CTA 197  
 GAGT T G AT AA TTTACC AA A T T C A T AA AAA T CAAA CT

Sbjct: 18916 GAGTATTGCAAT-AATTTTACCTTAAA-ATTGTTCAAA-TAAAAAAAATAACAAAACTA 18972

Query: 198 GTAGTCAGATCA-ATAAAATTCTACGTGGCAAAAAAAAAAAAA 238  
 GTAGTCA A CA A AAAATT CGTG AAAA A AAAA

Sbjct: 18973 GTAGTCAAAACCAGACAAAATTGC-CGTGAAAAAAGCAGAAAA 19013

>F54B3 [Full Sequence] [AceBrowser] ACC=Z48583  
 Length = 33,200

Plus Strand HSPs:

Score = 152 (22.8 bits), Expect = 0.85, P = 0.57

Identities = 118/186 (63%), Positives = 118/186 (63%), Strand = Plus / Plus

Query: 49 TCTCAATTGGCAACTGTCT-ATTATCCATTCCGCAATCACATT--TCGGATGTTCTCGAA 105  
 TCTCAAT G AA TG CT AT ATC AT GCAAT A TT TCG A T T A

Sbjct: 25833 TCTCAAT--G-AA-TGGCTGATAATCTATGT-GCAATGATTTTGATCGAAAAATG-TATTA 25886

Query: 106 AAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGA--GT-TCGTC-ATGAAGTTTACCC 161  
 AA ACTTCCCA TT T GA ACT A A GT T TC AT AA TTTACC

Sbjct: 25887 AAT-ACTTCCCACT-TT-TCAGAAAACTAACAGATTCCGTGTATTCTATAAA-TTTACCT 25942

Query: 162 AAAGGACTTTACTATGTGAA-TTAAATTGTCAAAGTAGTACAGATC-AAT-AAAATTC 218  
 AA A TT A T T TG A TT A TCAA T GTA C TC AAT AAAATTC

Sbjct: 25943 CAACTAATTCATTTTGTAGTTCTACC-TCAATATTGTACCCGCCCTCCAATCAAATTC 26001

Query: 219 TACGTGGCAAAAAAAA 234  
TACGT AA AAAAA  
Sbjct: 26002 TACGTCAGAATAAAAA 26017

## Minus Strand HSPs:

Score = 142 (21.3 bits), Expect = 2.4, P = 0.91

Identities = 88/141 (62%), Positives = 88/141 (62%), Strand = Minus / Plus

Query: 234 TTTTGTGTCACGTAGAAATTTTATTGATC-TGACTACTAGTTTGACAATTTAATTCACA 176  
TTTTTTTGGCC C A AATTT A T AT T TA T GTT GA TTTAA C CA  
Sbjct: 11113 TTTTGTGTCACCAAAAAATTTCAATTATTAATTTTATTGTTGGATTTTTAAACACCCA 11172

Query: 175 TA-GTAAAGTCCTTTGGGTAACTTCATGACGAACCTTTTCACAGTACTCCAATAACTTT 117  
A G AAA TT G T TT T A AA T TTTC CA TA T CAA AA TTT  
Sbjct: 11173 AAAGCAAAAAATTTACGTTTTTTTTTCT-AT-AA-T-TTCCCAATAATTCAA-AA-TTT 11226

Query: 116 GGG-A-AGTCC-TTTTCGAGAACATC 94  
G G A A C TTTTC GAACA C  
Sbjct: 11227 GTGTACAAACAATTTTCAGGAACAAC 11252

>C03A7 [Full Sequence] [AceBrowser] ACC=AF016451  
Length = 41,609

## Plus Strand HSPs:

Score = 152 (22.8 bits), Expect = 0.85, P = 0.57

Identities = 92/139 (66%), Positives = 92/139 (66%), Strand = Plus / Plus

Query: 95 ATGTTCTCGAAAAGGACTTCCCA-AAGTTATTGGAGTACTGTGAAAGAGT-TCGTGAT-G 151  
ATGTT T G AA GG TT C A AAG A TG T T TGAAA AGT T G CAT G  
Sbjct: 11864 ATGTTATTGTAA-GG--TTACTAGAAGGAAGTGTTTTTTTTGAAGAAAGTATAGACATTG 11920

Query: 152 AAGTTTACCCAAAGGA--CTTTACTATGTGAATTAATTTGTCAACTAGTAGTCAGATC 208  
A GT T C CAA G CTTTA TAT T AATTAAA TTGT C T G AG T  
Sbjct: 11921 ACGTCT-CTCAATGTTTCTTTAATAT-T-AATTAAAATTGTTTTCATTTTGAAAGTTT 11977

Query: 209 --AA-TAAAATT-CTACGTGGCAAA 229  
AA T AAATT CTACGTGGCAAA  
Sbjct: 11978 TAAAATCAAATTTCTACGTGGCAAA 12002

>ZK287 [Full Sequence] [AceBrowser] ACC=Z70757  
Length = 39,874

## Minus Strand HSPs:

Score = 149 (22.4 bits), Expect = 1.2, P = 0.69

Identities = 135/234 (57%), Positives = 135/234 (57%), Strand = Minus / Plus

Query: 234 TTTTGTGTCACG-TAGAAATTTTATTGATCTGACTACTAGTTTGACAATTTAATTCACA 176  
T TTTT T C AC T GA TTTT TTG T CTACT TT CA T TCACA  
Sbjct: 20947 TATTTTATACTACCCCTTGATTTT-TTG-TAAACCTACTTCTTAAGCAGAGTCTCTCACA 21004

Query: 175 TAGTAAAGTCCTTTGGGTA-AACTTCATGACGAACCTCT-T-TC-ACAGTACTCCAATAAC 120  
T GT CTTT TA AAC T AT A A TC T TC AC G A T AA AAC  
Sbjct: 21005 CT-T---GTTCTTTTATAGAACCT-ATTATCATTTCCATCTCTACCGGAATAGAAGAAC 21059

Query: 119 TTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAATGGATAATAGACAGTT 60  
T A T CTT GA ATC GAAAT AT G GGAAT AAT G C GTT  
Sbjct: 21060 CGTTCACATTTCTTAGTGACTCGATC-GAAATAATATCGAGGAATATTGAATGGCCCGTT 21118

Query: 59 GCCAATTGAGAGAAGACTGTTGCATCCGCCGCCGTGATT--TCCTCCCAAAAAAAAAAAAA 2  
GCCAATTG G GA GTT CA CG TG TT T TCC AAAAAA AAA  
Sbjct: 21119 GCCAATTGCTGGTGAA-GTT-CACACGATTTTCTGGTTGGTTTTCCTAAAAAATTAAT 21176

Query: 1 A 1  
A  
Sbjct: 21177 A 21177

>Y22D7AL [Full Sequence] [AceBrowser] ACC=AC084153  
Length = 89,370

Minus Strand HSPs:

Score = 147 (22.1 bits), Expect = 1.4, P = 0.76  
Identities = 99/156 (63%), Positives = 99/156 (63%), Strand = Minus / Plus

Query: 238 TTTTTTTTTTTTGCCACGTAGAAATTTATTGATCTGACTACTAGTTTGACAATTTAATTC 179  
TTTTTTTTTTTT A GT AATTTT TT TCTGA T T TT GA AATT AA  
Sbjct: 53522 TTTTTTTTTTTTAAATGTCAAATTTTTTT--TCTGAATTTT--TTCGAAAAATAAAAAA 53577

Query: 178 ACATAGTAAAG-TCC-TT-TGG-GTAAACTTCATGACGAACTCTTTC-ACAGTACTCCAA 124  
C T TAAA TC TT T GTAAA ATG CG A T T T A A TA T AA  
Sbjct: 53578 TCCTCCTAAAAATCAATTATTTCAGTAAAAA--ATGTCGGAATTTATATATA-TA-TGGAA 53633

Query: 123 TAACTTTGGGAAGTCCTTTTCGAGAACATCC-GAAATGTGAT 83  
AA TT GA T TTTTCG GAA A CC GAAA G GAT  
Sbjct: 53634 GAAATTATTGATTT--TTTTCGGGAAAAACCTGAAAAGCGAT 53673

>Y11D7A [Full Sequence] [AceBrowser] ACC=AL032632  
Length = 57,337

Plus Strand HSPs:

Score = 146 (21.9 bits), Expect = 1.6, P = 0.80  
Identities = 112/181 (61%), Positives = 112/181 (61%), Strand = Plus / Plus

Query: 45 CTTCTCTCAATTGGCAACTGTCTATTATCC-ATTCCGC--AA-TCACATTTCCGATGTTC 100  
CTTCT TCAA G CAACTGTCTAT AT C ATT C AA T A TTTCG TGTT  
Sbjct: 4520 CTTCT-TCAACCGCCAACGTGTCTATAATTGCTTTGCTTAAATTAT-TTTCGACTGTT- 4576

Query: 101 TCGAAAAGGACTTCCCAA-AG-T-TATTGGAGTACTGTGAA-AGA-GTTCGTCATG-A-A 153  
TC A A G C T AA AG T TATTGGA T TG AA A A G TC TC TG A A  
Sbjct: 4577 TCAAGATGTTTCATATAAACAGATCTATTGGAATTTTGACAACAAACGCTC-TC-TGTATA 4634

Query: 154 GTTTACCCAAAGGACTTTACTAT-GTGAATTAAATTGTCAAACCTAGTAGTCAGATCA-AT 211  
TTTA A A A TT C AT GT TTAA TT AAA G A CA A CA AT  
Sbjct: 4635 TTTTAGAAAGATTAAATTCCAATAGTTC-TTAATTTAAAAAAACGAATGCAAAACACAT 4693

Query: 212 AAAATTC 218  
A TTC  
Sbjct: 4694 GATTTTC 4700

>C46B10 [Full Sequence] [AceBrowser] ACC=AF039710  
Length = 20,237

## Plus Strand HSPs:

Score = 145 (21.8 bits), Expect = 1.8, P = 0.83

Identities = 55/79 (69%), Positives = 55/79 (69%), Strand = Plus / Plus

Query: 38 CAACAGTCTTCTCTCAATTGGCAACTGTC-TATTATCCATTCCGCAATCACATTTCCGAT 96  
CAAC G TT TCTCAATTGGCA TGTC TATT T CATT CA C CA T CGG T  
Sbjct: 14038 CAAC-GCGTTTCTCTCAATTGGCACTTGTCGTATT-TGCATTTA-CACACTCAGT-CGCTT 14093

Query: 97 GTTCTCGAAAAGGACTTCCC 116  
TC C AA AG ACTTC C  
Sbjct: 14094 TCTCACAAACAGTACTTCGC 14113

>F23H11 [Full Sequence] [AceBrowser] ACC=AF003389  
Length = 30,510

## Plus Strand HSPs:

Score = 144 (21.6 bits), Expect = 2.0, P = 0.86

Identities = 76/118 (64%), Positives = 76/118 (64%), Strand = Plus / Plus

Query: 47 TCTCTCAA-TTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCCGGA-TGTTCTCGA 104  
TC CTCAA TTGGCAA G C A AT T CCGCAA C TTT A TGTT C GA  
Sbjct: 1371 TCACTCAAATTGGCAA--G-C-AGCATGGCT-CCGCAAAG-C-TTTGAAAGTGTTTCGTGA 1423

Query: 105 AAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAA 164  
AA GA TTCCCAAAGTTA TACT T A GA T ATG GTTTAC CAAA  
Sbjct: 1424 CAAAGAATTCCCAAAGTTAAATGTTACTTTTCATGAAAAAATAATGT-GTTTACTCAA 1482

>T24C4 [Full Sequence] [AceBrowser] ACC=AF100306  
Length = 31,917

## Plus Strand HSPs:

Score = 144 (21.6 bits), Expect = 2.0, P = 0.86

Identities = 76/118 (64%), Positives = 76/118 (64%), Strand = Plus / Plus

Query: 47 TCTCTCAA-TTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCCGGA-TGTTCTCGA 104  
TC CTCAA TTGGCAA G C A AT T CCGCAA C TTT A TGTT C GA  
Sbjct: 31288 TCACTCAAATTGGCAA--G-C-AGCATGGCT-CCGCAAAG-C-TTTGAAAGTGTTTCGTGA 31340

Query: 105 AAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAA 164  
AA GA TTCCCAAAGTTA TACT T A GA T ATG GTTTAC CAAA  
Sbjct: 31341 CAAAGAATTCCCAAAGTTAAATGTTACTTTTCATGAAAAAATAATGT-GTTTACTCAA 31399

>Y53H1A [Full Sequence] [AceBrowser] ACC=AL132864  
Length = 27,963

## Minus Strand HSPs:

Score = 143 (21.5 bits), Expect = 2.2, P = 0.89

Identities = 71/117 (60%), Positives = 71/117 (60%), Strand = Minus / Plus

Query: 235 TTTTTTTTGGCCACGTA-GAATTTTATTGATCTGACTACTAGTTTGACAATTTAATTCAC 177  
 TTTTTTTTGC A A G TTTT TT AT TGA T TAGTTT ACAATTT A  
 Sbjct: 10404 TTTTTTTTGCACAAAAAAGGCTTTTTTT-ATTGAATTTTAGTTTACAATTTTCGAGAA 10462

Query: 176 ATAGTAAAGTC-CTTTGGGTAAACTTCATGA-CGAACTCTTTCACAGTACTCCAATAA 121  
 AT G AAA TC C TT T A TT T A CGAA TT A A T T A TAA  
 Sbjct: 10463 ATTGAAAATTCACATTTTATGGAATTTTAAATCGAAAAATTGAAATTTTAAACTAA 10520

>T07C12 [Full Sequence] [AceBrowser] ACC=Z73976  
 Length = 33,482

Minus Strand HSPs:

Score = 143 (21.5 bits), Expect = 2.2, P = 0.89

Identities = 105/176 (59%), Positives = 105/176 (59%), Strand = Minus / Plus

Query: 238 TTTTTTTTTTTGGCCACGTAGAAATTTTATTGATCTGACTACTAGTTTGACAAT-TTAATT 180  
 TTT TTTT T CC C T GA T T T G C T TTG T TT ATT  
 Sbjct: 30677 TTTAGTTTTCTCCCTCATTGACCTCTCGAAGTGAGCCGTTTCCGTTGTGTTTGTGATT 30736

Query: 179 CACATAGTAAAGTCCTTTGGGTAAACTTCAT-GA--CGAACTCTTTCACAGTACTCCAAT 123  
 CA A TAA GTCC T T CTTCA GA CGAACTCTTTC C GT AA  
 Sbjct: 30737 ATCA-ACTAAGGTCCGTATCTTC--CTTCAGAGATGCCGAATCTTTCGCCGTGAGATAAG 30793

Query: 122 AACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCG-GAATGGATAATAGAC 64  
 ACTTT G AAG C TTTTC AGA AT G ATGTG TT G GAA G A AA A AC  
 Sbjct: 30794 CACTTTCGAAAGAC-TTTTCTAGAGGATAAGTGATGTG-TTAAGAGAA-G-A-AACAAAC 30848

Query: 63 A 63  
 A  
 Sbjct: 30849 A 30849

>B0285 [Full Sequence] [AceBrowser] ACC=Z34533  
 Length = 41,397

Minus Strand HSPs:

Score = 143 (21.5 bits), Expect = 2.2, P = 0.89

Identities = 121/201 (60%), Positives = 121/201 (60%), Strand = Minus / Plus

Query: 237 TTTTTTTTTTTGGCCACGTAGAAATTTTATTGA-TCTGACTACT-AGTTTGACAATTTAAT- 181  
 TT TTT T TGC AC TAGAA AT GA T GA A T A TTT AA T AAT  
 Sbjct: 11406 TTGTTTCCTCTGTC-AC-TAGAAGGCGATGGACTAGGATCAGTGACTTTTCTGAAAT-AATG 11462

Query: 180 TCACATAGTAAAGTCCTTTGG-GTAAACTTCATGACGAA--CTCTTTCACAGT-ACTCCA 125  
 T A AT A A TC TT G A A T ATG AA CTCT T A G ACTCCA  
 Sbjct: 11463 TTAAATTTCAGAAATCTTTAAATGGAGAATAAATGTTAAACCTCTGTAATCGCGACTCCA 11522

Query: 124 ATAA-CTT-TGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGC----GGAATGGAT 71  
 TA CTT T G A TCCTTTTCGAG CATCC A T ATT C GGAA GGAT  
 Sbjct: 11523 -TATCTTGTTCGTATTCTTTTCGAGCGCATCCACGGATTATTCCACATGGAAGGGAT 11581

Query: 70 AATAGACA-GTT-GC--CAATTGAG 50  
 ATA A GTT GC CAATTG G

Sbjct: 11582 TATACATTTGTTCCGCTCAATTGGC 11606

>F10G2 [Full Sequence] [AceBrowser] ACC=U64836  
Length = 26,539

Plus Strand HSPs:

Score = 142 (21.3 bits), Expect = 2.4, P = 0.91

Identities = 90/144 (62%), Positives = 90/144 (62%), Strand = Plus / Plus

Query: 81 CAATCACATTTCCGATGTTCT-CGAAAAGGACTTCCCAAAGTTATTGGAG-TACTGTGAA 138  
CA TC CA C ATGTT C AAA AC TCC AA TT G G T C G GAA  
Sbjct: 8787 CATTCCCAAA-CAAATGTTCCCACTGAAAT-ACGTCCAAATACGGTTAGTGCTCCAG-GAA 8843

Query: 139 A-GAGTTCGTCATGAAGTTTACCCAAAGGACTTT-ACTATGTGAAT-TAAATTGTCAAAC 195  
GA TCATGA G TTA AAAGGA T A TA T AA T A TT T AAA  
Sbjct: 8844 CTGAAAAA-TCATGAGGCTTAAAAAAAGGAAAATCATTAGATCAACCTCAGTT-TGAAAG 8901

Query: 196 TAGTAGTCAGATCAATAAAATTCTACGTG 224  
TA AGTCA ATCAATAAAAT TA GTG  
Sbjct: 8902 TAAAAGTCATATCAATAAAATA-TA-GTG 8928

>Y48G1A [Full Sequence] [AceBrowser] ACC=AC024792  
Length = 43,096

Plus Strand HSPs:

Score = 142 (21.3 bits), Expect = 2.4, P = 0.91

Identities = 70/119 (58%), Positives = 70/119 (58%), Strand = Plus / Plus

Query: 116 CAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTA 175  
CA GT A TGA TA G GAA G GT CG C GA GTT A AAG A A A  
Sbjct: 16256 CAGGGTGAATGGAATAAGGAGAA-GCGTACGGCG-GATGTTGAGAAGAAGAAGGACAAGA 16313

Query: 176 TGTGAATTAAATTGTCAAACCTAGTAGTCAGATCAATAAAATTCTACGTGGCAAAAAAAA 234  
T A TTAAAT TC A T T GT G T AA A A T TA TGGCAAAAAAAA  
Sbjct: 16314 AATAATTTAAATTTTCCTATTTTTTGTGTTGTTGAAAATGACTTTATTTGGCAAAAAAAA 16372

>P56G4 [Full Sequence] [AceBrowser] ACC=Z81552  
Length = 38,062

Minus Strand HSPs:

Score = 141 (21.2 bits), Expect = 2.7, P = 0.93

Identities = 99/158 (62%), Positives = 99/158 (62%), Strand = Minus / Plus

Query: 238 TTTTTTTTTTTTGCCACGTAGAATTTTATTGATCTGA-CTACTAGTTTGA-CAATTTAAT 181  
TTT T TTTT AC AGAATTTTATTGAT T CTAC AGTTT A C ATTT T  
Sbjct: 20506 TTTATCGATTTTAAAC--AGAATTTTATTGATTTTTTCTAC-AGTTTTATCGATTTT-T 20561

Query: 180 TCACATAGTAA-AGTCCTTTGGG-TAAACTTCATGACGAACCTTTTACAGTACTCCAAT 123  
T ACA A T A T TTT TA A TT T CGA T TTT ACAG A T A T  
Sbjct: 20562 TAACAGAAATTTATTGATTTTTTCTACAGTTT-TATCGATTT-TTTAACAGAAATTTATT 20619

Query: 122 AACTTTGGG-A-AGTCCTTTTCGAGAAC-ATCCGAAATGTGATTG 81

A TTT A AGT TT TCGA A CCGAA T T ATTG  
 Sbjct: 20620 GATTTTTTCTACAGTT-TTATCGATTTTAAACCGAATTTT-ATTG 20662

Score = 141 (21.2 bits), Expect = 2.7, P = 0.93

Identities = 99/158 (62%), Positives = 99/158 (62%), Strand = Minus / Plus

Query: 238 TTTT TTTT AC AGAATTTTATTGAT T CTAC AGTTT A C ATTT T 181

Sbjct: 20720 TTTATCAATTTTAAAC--AGAATTTTATTGATTTTCTAC-AGTTTATCGATTTT-T 20775

Query: 180 TCACATAGTAA-AGTCCTTTGGG-TAAACTTCATGACGAACCTTTTCACAGTACTCCAAT 123

Sbjct: 20776 TAACAGAATTTTATTGATTTTCTACAGTTT-TATCGATTT-TTTAACAGAATTTTATT 20833

Query: 122 AACTTTGGG-A-AGTCCTTTTCGAGAAC-ATCCGAAATGTGATTG 81

Sbjct: 20834 GATTTTTTCTACAGTT-TTATCGATTTTAAACCGAATTTT-ATTG 20876

Score = 141 (21.2 bits), Expect = 2.7, P = 0.93

Identities = 99/158 (62%), Positives = 99/158 (62%), Strand = Minus / Plus

Query: 238 TTTT TTTT AC AGAATTTTATTGAT T CTAC AGTTT A C ATTT T 181

Sbjct: 21063 TTTATCGATTTTAAAC--AGAATTTTATTGATTTTCTAC-AGTTTATCGATTTT-T 21118

Query: 180 TCACATAGTAA-AGTCCTTTGGG-TAAACTTCATGACGAACCTTTTCACAGTACTCCAAT 123

Sbjct: 21119 TAACAGAATTTTATTGATTTTCTACAGTTT-TATCGATTT-TTTAACAGAATTTTATT 21176

Query: 122 AACTTTGGG-A-AGTCCTTTTCGAGAAC-ATCCGAAATGTGATTG 81

Sbjct: 21177 GATTTTTTCTACAGTT-TTATCGATTTTAAACCGAATTTT-ATTG 21219

Score = 138 (20.7 bits), Expect = 3.7, P = 0.97

Identities = 78/122 (63%), Positives = 78/122 (63%), Strand = Minus / Plus

Query: 238 TTTT TTTT AC AGAATTTTATTGAT T CTAC AGTTT A CAATTT T 181

Sbjct: 20677 TTTATCGATTTTAAAC--AGAATTTTATTGATTTTCTAC-AGTTTATCAATTTT-T 20732

Query: 180 TCACATAGTAA-AGTCCTTTGGG-TAAACTTCATGACGAACCTTTTCACAGTACTCCAAT 123

Sbjct: 20733 TAACAGAATTTTATTGATTTTCTACAGTTT-TATCGATTT-TTTAACAGAATTTTATT 20790

Query: 122 AACTTT 117

Sbjct: 20791 GATTTT 20796

>W03B1 [Full Sequence] [AceBrowser] ACC=U58753  
 Length = 38,152

Plus Strand HSPs:

Score = 141 (21.2 bits), Expect = 2.7, P = 0.93

Identities = 131/223 (58%), Positives = 131/223 (58%), Strand = Plus / Plus

Query: 1 TTTT TTTT GGA AAATCA C CG C GA GC A AGTC A T 55

Sbjct: 18749 TGT TTTT TTTT TGGAAAAAATCAACATTTTTCGACCGAAGCCA-AGTCAAGAAA-ATT 18806



Query: 56 TGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCC 115  
TG AACT T ATT T AATCA ATTT T T CG A A TTCC  
Sbjct: 18807 TGAAAACCTTTAGATTTTTCCTCAAAAAATCAAATTTACC-TCTAAACGTTATATA-TTCC 18864

Query: 116 CAAAGTTATTGGAGTACT-GTGAAGAGTTTCG-TCATGAAGTTT-ACCCAAAGGACTTTA 172  
AGT T G AG ACT GTGAAA A T C T A G A TTT A CCAAAG A T A  
Sbjct: 18865 TCGAGTCCTCG-AG-ACTAGTGAAAAATGCACTGAAGCAATTTTCAGCCAAAGTA-TGAA 18921

Query: 173 CTATG-TGAATTAAATTGTCAAACCTAGTAGTCAG-ATC-AATAAAATTCTA 220  
C ATG T A A T T AC AGT GT A ATC AATAA AT C A  
Sbjct: 18922 C-ATGATCTACCCATTCTTTGCACAAGTTGTAAACATCTAATAATATGCGA 18971

>Y48A6B [Full Sequence] [AceBrowser] ACC=AL023844  
Length = 75,073

Plus Strand HSPs:

Score = 141 (21.2 bits), Expect = 2.7, P = 0.93  
Identities = 79/117 (67%), Positives = 79/117 (67%), Strand = Plus / Plus

Query: 116 CAAAGTTATTGGAGTACTGTGAAGAGTTTCGTCATGAAGTTTACC-CAAAGGACTTTACT 174  
CAA GTT TT A T T T AAA AGTT AT AGTT A C C A GGA TTT CT  
Sbjct: 8650 CAAGGTT-TTATAATT-TAT-AAA-AGTTAA--ATACAGTTAAACACTAGGGATTTTGCT 8703

Query: 175 --ATGTGA-ATTAAATTGTCAAACCTAGT-AG-TCAGATCAATAAAATTCTACGTGGCAAA 229  
A TGA A AAAT G AAATA A T AGAT AATAAAATTCT CG G AAA  
Sbjct: 8704 TGAATGATAGAAAATAGA-AACTAAACATATAAGATTAATAAAATTCTTCGAGAAAAA 8762

Query: 230 AAA 232  
AAA  
Sbjct: 8763 AAA 8765

>T24C12 [Full Sequence] [AceBrowser] ACC=U41037  
Length = 18,633

Plus Strand HSPs:

Score = 140 (21.0 bits), Expect = 3.0, P = 0.95  
Identities = 92/150 (61%), Positives = 92/150 (61%), Strand = Plus / Plus

Query: 89 TTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAAGAGTTTCGTC 148  
TT CG A GTTCT GAA A A CC AAA AT G A T CTG GAAA TT T  
Sbjct: 16285 TTGCGAAAGTTCTTGAAGATCAG--CCGAAAC--ATCGAA-TGCTG-GAAAATTTTTTTTG 16338

Query: 149 ATGAAGTTTACCCAAAGGACTTTACTA--TG-TGAATTAAATTGTCAAACCTAGTAGTCAG 205  
TG A AAAG ACTT A TA TG T AA AAATTGTC AA T A  
Sbjct: 16339 CTGTTTCGGAAGAAAAAGAACTTGAATAAATGCTAAAAAAATTTGTCCAAATTCAACAATT 16398

Query: 206 ATCAATAAAA-TTCTACGTGGCAAAAAAAAAAAAA 238  
TC TAAAA TTC ACG G CAAAAAAAAAAAA A  
Sbjct: 16399 TTCC-TAAACCTTC-ACGGGTCAAAAAAAAAAACA 16430

>F21D5 [Full Sequence] [AceBrowser] ACC=Z54271  
Length = 21,173

## Minus Strand HSPs:

Score = 140 (21.0 bits), Expect = 3.0, P = 0.95

Identities = 76/122 (62%), Positives = 76/122 (62%), Strand = Minus / Plus

Query: 238 TTTTTTTTTTTGCCACGTAGAAATTTATTGATCTGACTACT-AGT-TTGACAATTTAAT 181  
 TTT TTTTTT C CG AGAATTTTATT AT T CTACT A T TT A ATTT  
 Sbjct: 3089 TTTCTTTTTTTTCTCCG-AGAATTTTATT-ATTTAGCTACTTAATATTTATTATTGTC 3146

Query: 180 TCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACTCCAATAA 121  
 TCA A GT TCC TG T CTT T G CT TTTC C T T CAATAA  
 Sbjct: 3147 TCAAAACGTTTT-TCCAGTGATTTCTCTTTTCT-GT-CT-TTCTCTTTCTTGAATAA 3202

Query: 120 CTTT 117  
 TTT  
 Sbjct: 3203 TTTT 3206

>Y54R5A [Full Sequence] [AceBrowser] ACC=AL032643  
 Length = 27,774

## Minus Strand HSPs:

Score = 140 (21.0 bits), Expect = 3.0, P = 0.95

Identities = 128/212 (60%), Positives = 128/212 (60%), Strand = Minus / Plus

Query: 238 TTTTTTTTTTTGCCACGTA--GAATT-TTA--TTGA-TCTGACTA-CTAGTTTGACAAT 186  
 TTTTTTTT TG A A GA TT TTA TT TC A T CTAG TT CAA  
 Sbjct: 14778 TTTTTTTTTTCATGAAAAAGACCGATTGTGTTAAATTTGTCCAATTTTCTAGATTTTCAAG 14837

Query: 185 TTAATTCACATA-GTA-AAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACT 128  
 T A TTCA A A GT AAG C TT TA CT A ACGAACTCTTT A AG A T  
 Sbjct: 14838 TCATTTC A-AGACGTTCAAG-CGTTAAAATAG-CTCAAAAACGAACTCTTTGATAGCATT 14894

Query: 127 CCAATAACTT-TGGGAAGTCCTTTTCGAGAACA-TCC-GAAATGTGATT-GCGGAATGGA 72  
 C ATAA T T GA T C TC AGAA TC GAA T G TT G G AT A  
 Sbjct: 14895 CATATAAGTAGTCTGATTGTCAGATCCAGAAATGCTCTTGAACCTC-GTTTCGTCGTATC-A 14952

Query: 71 TAATAGACAGTTGCCAATTGAGAGAAGACTGTTGCA-TCC 33  
 AA AG TT CA TTGA A AAGA T T GCA TCC  
 Sbjct: 14953 CAA-AGTGTTTTATCAGTTGATACAAGA-TAT-GCAATCC 14989

>Y47D3A [Full Sequence] [AceBrowser] ACC=AL117202  
 Length = 199,814

## Plus Strand HSPs:

Score = 140 (21.0 bits), Expect = 3.0, P = 0.95

Identities = 96/162 (59%), Positives = 96/162 (59%), Strand = Plus / Plus

Query: 83 ATCACATTTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTG-AAAGA 141  
 A CA ATTTTCG T TT TC AAAA ACT C AAA TTA TG A T T T AAA A  
 Sbjct: 155690 AGCATATTTTCGACTATTTTCAAAAAAACTCTCAAAAATTAGTGCATTTTATTCAAAA 155749

Query: 142 GTTCGTCATGAAG-TTTACCCAAAGGACTT-TA-CT--ATG-TGAATT-AAATTGTCAA 194  
 T G AT A TTTA A G TT TA CT A TGA T AAATTGTCAA  
 Sbjct: 155750 AGTGGAATTCACCTTTATATATTGATTTTCTATCTGAAAAATGACTGCAAATTGTCAA 155809

Query: 195 CTAG-TAGTCAGATCAATAAAATTCTACG-TGG-CAAAAAAAA 234  
AG TA A ATCA AAA TT AC T CAA AAAAA  
Sbjct: 155810 A-AGCTACGAAAATCACCAAATTTTGACTATTTTCAACAAAA 155851

>ZK675 [Full Sequence] [AceBrowser] ACC=Z46812  
Length = 22,703

Minus Strand HSPs:

Score = 138 (20.7 bits), Expect = 3.6, P = 0.97  
Identities = 76/123 (61%), Positives = 76/123 (61%), Strand = Minus / Plus

Query: 141 TCTTTCACAGTACTCCAATAACTTTGG-GAAGTCCTTTTCGAGAACATCCGAA-ATG-TG 85  
TC TTCAC G A C AATAA TTG GAA TC TTCGAGAACAT AA A T  
Sbjct: 15318 TCATTCACTGAAAACAAATAAATTTGTAGAA-TCTCTTTCGAGAACATGAAAATAAACTT 15376

Query: 84 ATTGCGGAATGGATAATAGACAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCCGCCGT 25  
TT GGAA GA AA A ACA T AT A A A GA T T G AT CG G T  
Sbjct: 15377 TTTTGGGAAACGACAAAAACATATATATATATATA-GA-TATCG-ATACGGAGATT 15433

Query: 24 GATTTC 19  
GATT C  
Sbjct: 15434 GATTCC 15439

>ZK1025 [Full Sequence] [AceBrowser] ACC=AL022288  
Length = 40,589

Minus Strand HSPs:

Score = 138 (20.7 bits), Expect = 3.7, P = 0.97  
Identities = 118/208 (56%), Positives = 118/208 (56%), Strand = Minus / Plus

Query: 209 TGATCTGACTACTAGTTTGACAATTTA-ATTC-ACATAGTAAAGTCCTTTGGGTAAACTT 152  
TG TCTGA A A TG CA TT A ATT ACA AGT A T TT T A  
Sbjct: 423 TGTCTGATAAACACAATGTCACTTGATATTAGACAGAGTTTAATA-TTACTCTCACGAG 481

Query: 151 CATGACGAACTCT-TTCACAGTACTCCAATAACTTTGGGAA-GTCCTTTTCGAGAACATC 94  
CA A AACTC TTCA A A T A TA TT G A G CC T C A ATC  
Sbjct: 482 CAATAAAAACTCGGTTTCAGAAAAGTAACTATGTTTCGAAATTGACCGGT-CATCCAGATC 540

Query: 93 CGAAATGTGATTG-CGGAATGGATAATAGACAGTTGCCA-ATTGAGAGAAGACTGTTGCA 36  
CGAA T G TT CGG G TA T C TTG A ATTG AG AGACT T A  
Sbjct: 541 CGAACTTGTTTTACGGCTCCGCTACTCT-CT-TTGAGACATTGTTAGGAGACTTCTCGA 598

Query: 35 TCCGCC-GCCGTGATTTCTCCCAAAAAAAAA 4  
CC C G C ATTTCC C CAAAAAAAA  
Sbjct: 599 GCCACATGTCAC-ATTTCCACTCAAAAAAAAA 630

>D1065 [Full Sequence] [AceBrowser] ACC=AF016414  
Length = 21,095

Minus Strand HSPs:

Score = 137 (20.6 bits), Expect = 4.0, P = 0.98

Identities = 117/197 (59%), Positives = 117/197 (59%), Strand = Minus / Plus

Query: 237 TTTTGTGTTTGGCA-CGTAGAATTTT-ATTGA-TCTGACTACTAGT-TTGACAATTTAA 182  
 TT T TTTT G A C G ATTT ATT T TGA TA T GT TTGA A T A  
 Sbjct: 10830 TTGTGTTTGGGAGAGCACCAGCAATTTTATTCTGTTTGA-TAATTGTATTGA-ATGTGAG 10887

Query: 181 TTCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACTCCAAT- 123  
 T CA AG A A T T AACT ATGAC A T T T ACAGTACTCCA  
 Sbjct: 10888 TACAACGAGAATAATTATGAAAACAACTCAATGACTAGTTTGTACAGTACTCCAGCC 10947

Query: 122 AACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTCATTG-CGGAATGGATAATA-GA 65  
 AACT G G C T TT G G A T C AAAT T AT G C GAAT GA A A GA  
 Sbjct: 10948 AACTAATGTT-G-CATCTT-GTGTAAGTAC-AAATAT-ATCGTCAGAATAGAAACAACGA 11002

Query: 64 C-AGTTGCCAATTGAGAGAAGACTG 41  
 AGT G AA T GAA A TG  
 Sbjct: 11003 AGAGTGGG-AAGTCTCTGAAAATTG 11026

>LLC1 [Full Sequence] [AceBrowser] ACC=Z82277  
 Length = 35,920

Minus Strand HSPs:

Score = 137 (20.6 bits), Expect = 4.1, P = 0.98

Identities = 59/89 (66%), Positives = 59/89 (66%), Strand = Minus / Plus

Query: 178 ACATAGTAAAGTCCTTTGGGTAAACT-TC-AT-GACGAACTCTTTCACAGTACTCCAATA 122  
 ACAT T AAG C T GG AA T TC A GAC A T T TCA AG A C ATA  
 Sbjct: 8105 ACATCTTGAAGAGCATCCGA-AAGGTGTCCACCGACTAGAT-TCTCATAGCAACCGTATA 8162

Query: 121 ACTTTGGGAAGTCCTTTTCGAGAACATCCGA 91  
 ACTTTG AA CCTTTTCGAGAA A CCGA  
 Sbjct: 8163 ACTTTGCAAATGCCCTTTTCGAGAAGAGCCGA 8193

>Y71F9AR [Full Sequence] [AceBrowser] ACC=AC024853  
 Length = 50,768

Minus Strand HSPs:

Score = 137 (20.6 bits), Expect = 4.1, P = 0.98

Identities = 93/149 (62%), Positives = 93/149 (62%), Strand = Minus / Plus

Query: 145 GAACTCTTTCACAGTACTCCAATAACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGT 86  
 GAACTCT C T CTCC A TTT G A TC T GAG A A CCGAAATG  
 Sbjct: 17864 GAACTCTGCGTCTCTTCTCCCGCATTTTTGTAGATCTACGTAGAGCAAA-CCGAAATGA 17922

Query: 85 GA---T-TG-CGGAATGGATAATAG--ACAGTTGCCAA-TTGAGAGAAG-ACTGTTGCAT 35  
 GA T TG C ATG TAATAG A AGTTG AA TT AGA AA A T TTG AT  
 Sbjct: 17923 GACACTCTGACACCATGT-TAATAGGAAAAGTTGAAAAATTCAGAAAAACATTTTGTAT 17981

Query: 34 CCGCCGCGTGATTTCTCCCAAAAAAAAAAAAAA 1  
 GC T TTT T CCA AAAAAAAAAAAAAA  
 Sbjct: 17982 TAAATGCA-T--TTTGGTTCCACAAAAAAAAAAAAA 18012

>Y53F4B [Full Sequence] [AceBrowser] ACC=AL132949

Length = 227,206

## Plus Strand HSPs:

Score = 137 (20.6 bits), Expect = 4.1, P = 0.98

Identities = 79/131 (60%), Positives = 79/131 (60%), Strand = Plus / Plus

Query: 108 GGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGA 167  
G ACT CCA TT T GA TA TG GA AGAGTTC TC GAA TTT G A  
Sbjct: 177830 GAACTGGCCACT-TTCGTAGA-TAGTG-GACAGAGTTCTTCTGGAATTTTTTTTTTGGAA 177886

Query: 168 C--TTTACTATGTGAATTAAATTGTCAAAGTAGTAGTCAGATCAATAAAATTCTACGTGG 225  
TTT A TGAA AAATTG AA TA A T A A AA AAAAT TA G  
Sbjct: 177887 AAATTTGAAAAGTGAAG-AAATTGAAAATATATGAATAAAAAAAAAAAAATA-TATGAAT 177944

Query: 226 CAAAAAAAAAAAAA 238  
AAAAAAAAAAAAA  
Sbjct: 177945 AAAAAAAAAAAAAA 177957

>R10E11 [Full Sequence] [AceBrowser] ACC=Z29095  
Length = 32,458

## Plus Strand HSPs:

Score = 136 (20.4 bits), Expect = 9.0, P = 1.0

Identities = 54/78 (69%), Positives = 54/78 (69%), Strand = Plus / Plus

Query: 162 AAAGGACTTTACTATGTGAATTAAATTG-TCAAAGTAGTAGTCAGATCAATAA-AATT-C 218  
A AGG T T TAT TGA TTA G T AAAGTA A T A AT AA AA AATT C  
Sbjct: 18780 ACAGGTATGTTTTAT-TGATTTATGAAGATAAAGTATAAATAA-ATGAAAATAATTGC 18837

Query: 219 TACGTGGCAAAAAAAAAAAAA 238  
TACGTGGCAA A AAAA AA  
Sbjct: 18838 TACGTGGCAATACAAAACAA 18857

>P43C1 [Full Sequence] [AceBrowser] ACC=Z46937  
Length = 35,188

## Minus Strand HSPs:

Score = 136 (20.4 bits), Expect = 9.0, P = 1.0

Identities = 116/187 (62%), Positives = 116/187 (62%), Strand = Minus / Plus

Query: 216 ATTTTATTGATCTGACTAC-TAGTTTGACAATTTAATTCACA--TAGTAAAGTC-CTTTG 161  
ATTTTATT A T A TA TA TT A A TT ATTC C T GT A G C CTT  
Sbjct: 4126 ATTTTATTAAATTTATTAAATA-TTACAGTACTTGATTCCTGGTGGTGGTGCCTCTTCC 4184

Query: 160 GGTAAACTTCATGACGAAGTCTTTTACAGTACTCCAATAACTTTGGGAAGTCCTTTTCGA 101  
AAAC C T AC AACTCTTTCAC T T CAAT ACTTT G AA TC T C A  
Sbjct: 4185 ACAAAC--C-T-ACAACTCTTTCACCTTTCTTTCAATCACTTTTCGAAA-TC-TGC-C-A 4236

Query: 100 GAACATCCGAAATGTGATTGCG-GAATG-GATAATAGACAGTTGCCAATTGAGAGAAGAC 43  
GA T GA AT GATTGC GAAT GA A T C G GC AAT A A AG C  
Sbjct: 4237 GAT--TG-GATATCAGATTGCCCGAATTTGACATTTCTCCGA-GCAAATA-ATAATAGCC 4291

Query: 42 T-GTTGCATCCGCC 30  
T GT GCA C GCC

Sbjct: 4292 TTGTCCCA-CTGCC 4304

>C44H4 [Full Sequence] [AceBrowser] ACC=Z79598  
Length = 35,920

Minus Strand HSPs:

Score = 136 (20.4 bits), Expect = 9.0, P = 1.0

Identities = 116/200 (58%), Positives = 116/200 (58%), Strand = Minus / Plus

Query: 198 CTAGTTTGACAATTTAATTCACATAGTAAAGTC-CTTTGGGTAAACTTC--ATGACGAAC 142  
C A T T A C A T T A A C A T T A T C T T G T A C T T C A T G C A A C  
Sbjct: 3929 CAATTGTTACAGATTAACGCAGTTGATGATTTTGCCTCAGTCAGCTTCCTATG-CTAAC 3987

Query: 141 T-CT-TTCACAGTACTCCAATAA-CTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTG 85  
T C T T T A A T A T A C T T G A A T C T T C G A G A A T A A T G  
Sbjct: 3988 TTCTCTTGATTGAGT--AGTAATCGATTAGAA-TCATTACCGAGCA-ATGTTATATACG 4043

Query: 84 ATTGCGGAATGGATAATAGACAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCCGCC-G 26  
A T A T G A A A A A G T C C A T T A A G A A C T T T A T C G G  
Sbjct: 4044 ACTCATTGATGCAAAAGAAAACGTCACCAGTTCAAAGAAAAC-TTCAATTCAGAGTAAG 4102

Query: 25 TGAT-TTCCTCCCAAAAAAAAAAAAAA 1  
G A T T C C A A A A A A A A A A A  
Sbjct: 4103 AGAAATTCAAAACAAAAAAAAAAAAAGA 4128

## Parameters:

P=4

warnings

B=100

V=100

ctxfactor=2.00

E=10

Query	Strand	MatID	Matrix name	-----	As Used	-----	-----	Computed	-----
				Lambda	K	H	Lambda	K	H
	+1	0	+5,-4	0.192	0.173	0.357	same	same	same
			q=10 r=10	0.104	0.0151	0.0600			
	-1	0	+5,-4	0.192	0.173	0.357	same	same	same
			q=10 r=10	0.104	0.0151	0.0600			

Query	Strand	MatID	Length	Eff.Length	E	S	W	T	X	E2	S2
	+1	0	238	238	10.	136	11	N/A	73	0.023	74
										79	0.025 100
	-1	0	238	238	10.	136	11	N/A	73	0.023	74
										79	0.025 100

## Statistics:

Database: /data/blastdb/wormpub/allcmid  
Title: wormpub/allcmid  
Release date: unknown  
Posted date: 12:14 PM BST May 17, 2001  
Format: BLAST  
# of letters in database: 104,258,147

# of sequences in database: 3692  
# of database sequences satisfying E: 35  
No. of states in DFA: 180 (360 KB)  
Total size of DFA: 371 KB (384 KB)  
Time to generate neighborhood: 0.01u 0.01s 0.03t Elapsed: 00:00:00  
No. of threads or processors used: 4  
Search cpu time: 4.41u 1.80s 6.21t Elapsed: 00:00:31  
Total cpu time: 4.51u 1.83s 6.35t Elapsed: 00:00:32  
Start: Thu May 17 17:10:32 2001 End: Thu May 17 17:11:04 2001

script last modified Mon Apr 23 16:35:41 2001

[webmaster@sanger.ac.uk](mailto:webmaster@sanger.ac.uk)

## Figure 5

NIXON

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## Blast Server Results

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COMPAQ NonStopLow complexity filtering enabled  
Repeatmasker disabled

BLASTX 2.0a13MP-WashU [10-Jun-1997] [Build 23:08:19 Jun 10 1997]

Reference: Gish, Warren (1994-1997). unpublished.

Gish, Warren and David J. States (1993). Identification of protein coding regions by database similarity search. Nat. Genet. 3:266-72.

Notice: statistical significance is estimated under the assumption that the equivalent of one entire reading frame in the query sequence codes for protein and that significant alignments will involve only coding reading frames.

Query= gi  
(238 letters)

Translating both strands of query sequence in all 6 reading frames

Database: wormpub/wormpep\_current  
19,835 sequences; 8,675,472 total letters.

Searching....10....20....30....40....50....60....70....80....90....100% done

			Reading	High	Smallest	
			Frame	Score	Sum	
Sequences producing High-scoring Segment Pairs:					Probability	N
					P (N)	
F35E8.11	CE15961	Glutathione S-transferases. (HINX...	+1	296	9.2e-27	1
K01D12.12	CE06051	Glutathione S-transferases. (HINX...	+1	232	5.6e-20	1
K01D12.11	CE06050	Glutathione S-transferases. (HINX...	+1	229	1.2e-19	1
K01D12.13	CE06052	Glutathione S-transferases. (HINX...	+1	216	2.8e-18	1
C54D10.1	CE05497	Glutathione S-transferases. (HINX...	+1	215	3.5e-18	1
C54D10.2	CE05498	Glutathione S-transferases. (HINX...	+1	213	5.7e-18	1
K01D12.14	CE06053	(HINXTON)	+1	169	2.6e-13	1
C25H3.7	CE02505	(ST.LOUIS)	+1	153	2.6e-11	1
Y48C3A.3	CE22138	(HINXTON)	+1	97	5.4e-05	1
Y47H10A.1	CE24374	(HINXTON)	+2	61	0.0058	2
Y57A10A.26	CE22631	(HINXTON)	+1	74	0.015	1
C14C11.8	CE06827	(ST.LOUIS)	-1	43	0.48	2
Y5H2B.4	CE21318	(ST.LOUIS)	+2	58	0.65	1
R13D7.7	CE18153	(ST.LOUIS)	+1	52	0.67	2
F58H7.5	CE17933	(ST.LOUIS)	-1	57	0.68	1
Y41D4A.A	CE21846	(ST.LOUIS)	+2	54	0.71	2
T02E9.1	CE13062	G-protein coupled receptor (HINXTON)	+2	58	0.74	1
F32A5.2	CE01934	Peroxidase (ST.LOUIS)	-2	61	0.86	1
F23H12.5	CE05708	Thrombospondin type 1 domain (HIN...	-1	48	0.91	2
T04C9.4A	CE26618	(ST.LOUIS)	-1	48	0.94	1



T02G5.9	CE04861	lysyl-tRNA synthetase (ST.LOUIS)	+3	<u>56</u>	0.98	1
T04C9.4B	CE26619	(ST.LOUIS)	-1	<u>48</u>	0.98	1
W10G11.16	CE14830	channel protein (ST.LOUIS)	-2	<u>53</u>	0.98	1
K10D3.2	CE25055	locus:unc-14 (HINKTON)	-2	<u>56</u>	0.99	1
F40G12.4	CE10182	(HINKTON)	-2	<u>52</u>	0.99	1
F59E12.5	CE11526	(ST.LOUIS)	+3	<u>54</u>	0.996	1
C08E3.8	CE08011	(ST.LOUIS)	-1	<u>53</u>	0.996	1
F11G11.3	CE07056	Glutathione S-transferase (ST.LOUIS)	+1	<u>55</u>	0.998	1
C46E10.9	CE08767	zinc finger protein (ST.LOUIS)	-1	<u>52</u>	0.999	1
T04C9.4C	CE26620	contains LIM-like binding domain ...	-1	<u>48</u>	0.9994	1
Y22D7AR.3	CE23432	(ST.LOUIS)	+1	<u>45</u>	0.9996	1
F52A8.1	CE05908	(HINKTON)	-2	<u>46</u>	0.9997	1
ZK1037.6	CE16758	(HINKTON)	-2	<u>52</u>	0.9998	1

>F35E8.11 [[Full Sequence](#)] [[AceBrowser](#)] CE15961 Glutathione S-transferases. (HINKTON)  
Length = 277

Plus Strand HSPs:

Score = 296 (104.2 bits), Expect = 9.2e-27, P = 9.2e-27  
Identities = 56/58 (96%), Positives = 56/58 (96%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVREHVYPKDFTM 177  
F F EEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVREHVYPKDFTM  
Sbjct: 220 FLFGKEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVREHVYPKDFTM 277

>K01D12.12 [[Full Sequence](#)] [[AceBrowser](#)] CE06051 Glutathione S-transferases. (HINKTON)  
Length = 277

Plus Strand HSPs:

Score = 232 (81.7 bits), Expect = 5.6e-20, P = 5.6e-20  
Identities = 42/58 (72%), Positives = 49/58 (84%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVREHVYPKDFTM 177  
F F ++IT DATVF QLA+VYYP R+HI+DVLEKDFPK+LEYCE VR EVYP DFT+  
Sbjct: 220 FLFGDKITPTDATVFGQLASVYYPPLRSHINDVLEKDFPKILEYCESVRKEVYPNDFTI 277

>K01D12.11 [[Full Sequence](#)] [[AceBrowser](#)] CE06050 Glutathione S-transferases. (HINKTON)  
Length = 277

Plus Strand HSPs:

Score = 229 (80.6 bits), Expect = 1.2e-19, P = 1.2e-19  
Identities = 41/58 (70%), Positives = 50/58 (86%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVREHVYPKDFTM 177  
F F ++IT ADATVF QLATVYYP R+H++DVL+KDFPK+LEY ERVR E+YP DFT+  
Sbjct: 220 FLFGDKITPADATVFGQLATVYYPPIRSHLTDVLDKDFPKVLEYLERVRKEIYPNDFTI 277

>K01D12.13 [[Full Sequence](#)] [[AceBrowser](#)] CE06052 Glutathione S-transferases. (HINKTON)  
Length = 287

Plus Strand HSPs:

Score = 216 (76.0 bits), Expect = 2.8e-18, P = 2.8e-18  
Identities = 38/58 (65%), Positives = 45/58 (77%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 177  
+ F + I DATVFSQLA VYYPF HIS VLE DFPK+L+YCER+R E+YP DFT+  
Sbjct: 230 YLFGDHIAPVDATVFSQLAVVYYPFYTHISTVLENDFPKILQYCERIRKEIYPNDFTI 287

>C54D10.1 [Full Sequence] [AceBrowser] CE05497 Glutathione S-transferases. (HINXTON)  
Length = 278

Plus Strand HSPs:

Score = 215 (75.7 bits), Expect = 3.5e-18, P = 3.5e-18  
Identities = 38/58 (65%), Positives = 47/58 (81%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 177  
F F +++TAADA VF Q+A+V YPFR I+D LE DFPK+LEYCERVR E+YP DFT+  
Sbjct: 221 FLFGDKVTAADAAVFGQIASVIYPFRCSINDALENDFPKILEYCERVRQEIYPNDFTI 278

>C54D10.2 [Full Sequence] [AceBrowser] CE05498 Glutathione S-transferases. (HINXTON)  
Length = 315

Plus Strand HSPs:

Score = 213 (75.0 bits), Expect = 5.7e-18, P = 5.7e-18  
Identities = 39/56 (69%), Positives = 45/56 (80%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDF 171  
F F +E+ AADA VF QLTV YPFR I+D+LE DFP+LLEYCERVR E+YP DF  
Sbjct: 258 FLFGDEVKAADAAVFGQLATVIYPFRCKINDILENDFPQLLEYCERVRKEIYPNDF 313

>K01D12.14 [Full Sequence] [AceBrowser] CE06053 (HINXTON)  
Length = 250

Plus Strand HSPs:

Score = 169 (59.5 bits), Expect = 2.6e-13, P = 2.6e-13  
Identities = 27/58 (46%), Positives = 43/58 (74%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 177  
+ F ++IT+AD TVF ++A+ YYPF N S +++ +PKL EYC+R+ E+YP DF++  
Sbjct: 193 YLFGDKITSADCTVFGEVASAYYPFPNKPBRILDSHYPKLHEYCDRIIEELYPNDFSI 250

>C25H3.7 [Full Sequence] [AceBrowser] CE02505 (ST.LOUIS)  
Length = 275

Plus Strand HSPs:

Score = 153 (53.9 bits), Expect = 2.6e-11, P = 2.6e-11  
Identities = 26/55 (47%), Positives = 38/55 (69%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPK 165  
F F + IT+ D +VF Q+ V+Y P+R ISD+LE DFP++ YC+R+R YP+

Sbjct: 217 FLFGDRITSVDCSVFGQIGAVFYLPYRQQISDLLEDDFPRVRAYCDRIRQHYYPE 271

>Y48C3A.3 [Full Sequence] [AceBrowser] CE22138 (HINXTON)  
Length = 321

Plus Strand HSPs:

Score = 97 (34.1 bits), Expect = 6.4e-05, P = 6.4e-05  
Identities = 24/77 (31%), Positives = 41/77 (53%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLATVYY-PFRNHISDVLEKDFPKLLLEYCERVVRHEVYPKOPTM\* 180  
+F + T DA +FS L +YY P+ + D+++ + L EY ER+++ YP +  
Sbjct: 239 YFHGFKPTKVDACIFSHLCQIYYAPYTSEHRDLIDGECCKNLAHYVERIKNRFPDWDDVT 298

Query: 181 IKLSN\*\*SDQ\*NSTWQKK 234  
K S +D S W+K+  
Sbjct: 299 TKFS---TD--TSNWKKR 311

>Y47H10A.1 [Full Sequence] [AceBrowser] CE24374 (HINXTON)  
Length = 638

Plus Strand HSPs:

Score = 61 (21.5 bits), Expect = 0.0058, Sum P(2) = 0.0058  
Identities = 11/44 (25%), Positives = 23/44 (52%), Frame = +2

Query: 98 FSKRTSQSYWSTVKEFVMKFTQRTLLCELNCQTSSQINKILRGK 229  
F + +W ++K+P+++FT C L+ T ++ K+ K  
Sbjct: 419 FRIKEDGEFWMSLKDFMVEFTD-VYCCNLSADTMHEVEKMTFVR 461

Score = 43 (15.1 bits), Expect = 0.0058, Sum P(2) = 0.0058  
Identities = 10/17 (58%), Positives = 11/17 (64%), Frame = +3

Query: 21 NHGGGCNSLLSIGNCLL 71  
N GG NSL SIG +L  
Sbjct: 97 NMGGKTNSLSSIGKIVL 113

>Y57A10A.26 [Full Sequence] [AceBrowser] CE22631 (HINXTON)  
Length = 269

Plus Strand HSPs:

Score = 74 (26.0 bits), Expect = 0.016, P = 0.015  
Identities = 16/55 (29%), Positives = 28/55 (50%), Frame = +1

Query: 4 FFFWEEITAADATVFSQLAT-VYYP-FRNHISDVLEKDFPKLLLEYCERVVRHEVYP 162  
+ F I D T F+ LA +Y P F I +++ P ++EY R++ + +P  
Sbjct: 197 YLFGSSIKTIDVTAFAPHLAELIYTPQFSPIRAYIDEKVPNVMEYVIRIKEKYWP 251

>C14C11.8 [Full Sequence] [AceBrowser] CE06827 (ST. LOUIS)  
Length = 654

Minus Strand HSPs:

Score = 43 (15.1 bits), Expect = 0.66, Sum P(2) = 0.48  
Identities = 7/13 (53%), Positives = 7/13 (53%), Frame = -1

Query: 115 GSPFREHPKCDG 77  
G P P CDCG  
Sbjct: 113 GCPSSSPSCDCG 125

Score = 41 (14.4 bits), Expect = 0.66, Sum P(2) = 0.48  
Identities = 7/13 (53%), Positives = 9/13 (69%), Frame = -2

Query: 42 CCIRRRDFLPKKK 4  
CC+R+R L K K  
Sbjct: 641 CCLRKRHRLAKNK 653

>Y5H2B.4 [Full Sequence] [AceBrowser] CE21318 (ST. LOUIS)  
Length = 307

Plus Strand HSPs:

Score = 58 (20.4 bits), Expect = 1.0, P = 0.65  
Identities = 17/67 (25%), Positives = 31/67 (46%), Frame = +2

Query: 44 BSLNWQLSIHSITFRMFSSKRTSQSYWSTVKE--FVMKFTQRTLL-CELNCQT-SSQIN 211  
S N++L+I + +T YW+T K +++ F +L C+L + SQ N  
Sbjct: 158 SFCNFRLNIPYGCVTLSCSLNLCFYQYWFYKTYIVYILTFSLSTIVLTCKLLKIHESQSN 217

Query: 212 KILRGKK 232  
+ R +  
Sbjct: 218 NLTRANR 224

>R13D7.7 [Full Sequence] [AceBrowser] CE18153 (ST. LOUIS)  
Length = 273

Plus Strand HSPs:

Score = 52 (18.3 bits), Expect = 1.1, Sum P(2) = 0.67  
Identities = 13/33 (39%), Positives = 20/33 (60%), Frame = +1

Query: 94 DVLEKDFPKLLEYCERVVRHEVYPKDFTM\*IKLS 192  
D++ K P+ LE E + E++P DF + KLS  
Sbjct: 180 DMVNKTLPSLERLE-CQFEIHGDFIIGNKLS 211

Score = 34 (12.0 bits), Expect = 1.1, Sum P(2) = 0.67  
Identities = 6/8 (75%), Positives = 7/8 (87%), Frame = +3

Query: 12 LGGNHGGG 35  
LGG +GGG  
Sbjct: 33 LGGYYGGG 40

>F58H7.5 [Full Sequence] [AceBrowser] CE17933 (ST. LOUIS)  
Length = 272

Minus Strand HSPs:

Score = 57 (20.1 bits), Expect = 1.1, P = 0.68  
 Identities = 13/39 (33%), Positives = 19/39 (48%), Frame = -1

Query: 154 LHDLELFHSTPITLGSPFFREHPKCDGMDNRQLPIERRLL 38  
 L D L P + PFRE P+ D M Q P+++ +  
 Sbjct: 143 LEDPLRRRVFYELHFPFREFPPQEDAPHRMAQNPFVDQRAI 181

>Y41D4A.A [Full Sequence] [AceBrowser] CE21846 (ST.LOUIS)  
 Length = 347

## Plus Strand HSPs:

Score = 54 (19.0 bits), Expect = 1.3, Sum P(2) = 0.71  
 Identities = 10/27 (37%), Positives = 18/27 (66%), Frame = +2

Query: 23 SRRRMQQSSLNWQLSTIHSATFRMFS 103  
 + R M SS+NW L+++ ++ T +FS  
 Sbjct: 89 THRIMSGSSINWYLAVLSASDTLILFS 115

Score = 34 (12.0 bits), Expect = 1.3, Sum P(2) = 0.71  
 Identities = 11/33 (33%), Positives = 17/33 (51%), Frame = +2

Query: 125 WS-TVKEFVMKFTQRTLLCELNCQTSSQINKILR 223  
 W+ T+ +V+ FT LL LN S + + R  
 Sbjct: 244 WAYTIVMYVVPFT---LLTALNSMVL SAVRRSRR 274

>T02E9.1 [Full Sequence] [AceBrowser] CE13062 G-protein coupled receptor (HINXTON)  
 Length = 376

## Plus Strand HSPs:

Score = 58 (20.4 bits), Expect = 1.4, P = 0.74  
 Identities = 17/53 (32%), Positives = 22/53 (41%), Frame = +2

Query: 83 ITFRMFSEKRTS----QSYWSTVKEFVMKFTQRTLLCELNCQTSSQINKILRGKK 232  
 +T RM KRT + Y E KF L+C +C+ I GKK  
 Sbjct: 321 VTERMIRKRTKSMHRKGYSEAAVELTSKFDDVPLMCP-HCEAQLSIRSSSNGKK 373

>F32A5.2 [Full Sequence] [AceBrowser] CE01934 Peroxidase (ST.LOUIS)  
 Length = 977

## Minus Strand HSPs:

Score = 61 (21.5 bits), Expect = 2.0, P = 0.86  
 Identities = 10/26 (38%), Positives = 16/26 (61%), Frame = -2

Query: 81 AEWIIDSCQLREDCCIRRRDFLPKKK 4  
 A+W++D+CQL + C R+ P K  
 Sbjct: 61 ADWNVDNCQLACNTCTRKNVIRPATK 86

>F23H12.5 [Full Sequence] [AceBrowser] CE05708 Thrombospondin type 1 domain (HINXTON)  
 Length = 802

## Minus Strand HSPs:

Score = 48 (16.9 bits), Expect = 2.4, Sum P(2) = 0.91  
Identities = 8/17 (47%), Positives = 11/17 (64%), Frame = -1

Query: 112 SPFR~~E~~HPKCD~~C~~GMDNRQ 62  
SP+ E KC CG +R+  
Sbjct: 707 SPWSEWTKCQCGKQSRK 723

Score = 32 (11.3 bits), Expect = 2.4, Sum P(2) = 0.91  
Identities = 5/10 (50%), Positives = 7/10 (70%), Frame = -2

Query: 189 QFN~~S~~HSKVLW 160  
QF + KV+W  
Sbjct: 697 QFKNGKKVIW 706

>T04C9.4A [[Full Sequence](#)] [[AceBrowser](#)] CE26618 (ST.LOUIS)  
Length = 120

## Minus Strand HSPs:

Score = 48 (16.9 bits), Expect = 2.8, P = 0.94  
Identities = 14/32 (43%), Positives = 16/32 (50%), Frame = -1

Query: 166 PLGK~~L~~HDELPHSTPITLGSPFR--EHPKCD-CG 77  
PL L D H+ PF+ EHPKC CG  
Sbjct: 9 PLSHLTDPA-HTIFKVSSMPFKPVEHPKCPKCG 40

>T02G5.9 [[Full Sequence](#)] [[AceBrowser](#)] CE04861 lysyl-tRNA synthetase (ST.LOUIS)  
Length = 572

## Plus Strand HSPs:

Score = 56 (19.7 bits), Expect = 3.7, P = 0.98  
Identities = 11/25 (44%), Positives = 14/25 (56%), Frame = +3

Query: 39 NSLLSIGNCLLSIPQSHFGCSRKGL 113  
N +L + CL +P SHFG K L  
Sbjct: 180 NEILQLTPCLHNLPHSEHFGKDKREL 204

>T04C9.4B [[Full Sequence](#)] [[AceBrowser](#)] CE26619 (ST.LOUIS)  
Length = 138

## Minus Strand HSPs:

Score = 48 (16.9 bits), Expect = 3.8, P = 0.98  
Identities = 14/32 (43%), Positives = 16/32 (50%), Frame = -1

Query: 166 PLGK~~L~~HDELPHSTPITLGSPFR--EHPKCD-CG 77  
PL L D H+ PF+ EHPKC CG  
Sbjct: 9 PLSHLTDPA-HTIFKVSSMPFKPVEHPKCPKCG 40

>W10G11.16 [[Full Sequence](#)] [[AceBrowser](#)] CE14830 channel protein (ST.LOUIS)

Length = 327

## Minus Strand HSPs:

Score = 53 (18.7 bits), Expect = 4.0, P = 0.98  
Identities = 12/33 (36%), Positives = 19/33 (57%), Frame = -2

Query: 165 LWVNFMTNS--FTVLQ\*LWEVLFENIRNVIAEW 73  
LW F+T FT+LQ L+ + F+ N + +W  
Sbjct: 230 LWFGFITGPFVFFTLQLFVIGFDKRRANQLKKW 262

>K10D3.2 [Full Sequence] [AceBrowser] CE25055 locus:unc-14 (HINXTON)  
Length = 665

## Minus Strand HSPs:

Score = 56 (19.7 bits), Expect = 4.4, P = 0.99  
Identities = 11/31 (35%), Positives = 20/31 (64%), Frame = -2

Query: 111 VLFENIRNVIAEWIIDSCQLREDCCIRRRDF 19  
+LFE++ ++ +DS Q RE C +++ DF  
Sbjct: 35 MLFESVDPSPVSTDLSLDSQQFRERCQMKKEDF 65

>F40G12.4 [Full Sequence] [AceBrowser] CE10182 (HINXTON)  
Length = 294

## Minus Strand HSPs:

Score = 52 (18.3 bits), Expect = 4.4, P = 0.99  
Identities = 12/35 (34%), Positives = 20/35 (57%), Frame = -2

Query: 114 EVLFENIRNVIAEWIIDSCQLREDCCIRRRDFLPK 10  
E+L + +N ++ +S L+E+ C R DFL K  
Sbjct: 27 EILSDRTKNCFFKFF-ESVLLKENSCSRNPFDLAK 60

>F59E12.5 [Full Sequence] [AceBrowser] CE11526 (ST.LOUIS)  
Length = 527

## Plus Strand HSPs:

Score = 54 (19.0 bits), Expect = 5.5, P = 1.0  
Identities = 12/36 (33%), Positives = 16/36 (44%), Frame = +3

Query: 9 FLGCNHHGGGCSLLSIGNCLLSIPQSHFGCSRKGLP 116  
F G + GG ++ S G+C CS GLP  
Sbjct: 489 FSGSSSGSGRGAVWSCGHCTFQNEAGRQDCSMCGLP 524

>C08E3.8 [Full Sequence] [AceBrowser] CE08011 (ST.LOUIS)  
Length = 431

## Minus Strand HSPs:

Score = 53 (18.7 bits), Expect = 5.6, P = 1.0

Identities = 8/12 (66%), Positives = 9/12 (75%), Frame = -1

Query: 112 SPFREHPKDCG 77  
SPFR+ P C CG  
Sbjct: 147 SPFRQEPCTCTG 158

>F11G11.3 [Full Sequence] [AceBrowser] CE07056 Glutathione S-transferase (ST.LOUIS)  
Length = 235

Plus Strand HSPs:

Score = 55 (19.4 bits), Expect = 6.1, P = 1.0  
Identities = 15/52 (28%), Positives = 27/52 (51%), Frame = +1

Query: 4 FFFWEBITAADATVF---SQLATVYYPFRNHISDVLEKDFPKLLEYCERVH 150  
F F+E I A++ + F + L V H+ D+L+KD + E+ + + H  
Sbjct: 162 FEFFENILASNHSGFFVGNSLTWVDLLISQHVQDILDKDLAVVEEFKKVLAH 213

>C46E10.9 [Full Sequence] [AceBrowser] CE08767 zinc finger protein (ST.LOUIS)  
Length = 416

Minus Strand HSPs:

Score = 52 (18.3 bits), Expect = 6.8, P = 1.0  
Identities = 12/41 (29%), Positives = 19/41 (46%), Frame = -1

Query: 154 LHDELPHST-PITLGSPFREHPKDCGMDNRQLPIERRLLH 35  
+H +HST P L +P +E C D+ + + LH  
Sbjct: 341 IHVYVYHSTNPAQLQNPAQCQHCRIQFDDAPMSLEENALH 381

>T04C9.4C [Full Sequence] [AceBrowser] CE26620 contains LIM-like binding domain (ST.  
Length = 206

Minus Strand HSPs:

Score = 48 (16.9 bits), Expect = 7.4, P = 1.0  
Identities = 14/32 (43%), Positives = 16/32 (50%), Frame = -1

Query: 166 PLGKLHDELPHSTPITLGSPFR--EHPKCD-CG 77  
PL L D H+ PF+ EHPKC CG  
Sbjct: 9 PLSHLTDPA-HTIFKVSSMPFKPVEHPKCPKCG 40

>Y22D7AR.3 [Full Sequence] [AceBrowser] CE23432 (ST.LOUIS)  
Length = 65

Plus Strand HSPs:

Score = 45 (15.8 bits), Expect = 7.9, P = 1.0  
Identities = 7/17 (41%), Positives = 13/17 (76%), Frame = +1

Query: 115 PKLLEYCERVVRHEVYPK 165  
P++++YC R+ H + PK  
Sbjct: 29 PRIIDYCTRIFH-LSPK 44



>F52A8.1 [Full Sequence] [AceBrowser] CE05908 (HINXTON)  
Length = 110

Minus Strand HSPs:

Score = 46 (16.2 bits), Expect = 8.1, P = 1.0  
Identities = 7/21 (33%), Positives = 12/21 (57%), Frame = -2

Query: 75 WIIDSC-QLREDCCIRRRDFL 16  
W C Q+ + CC R +D++  
Sbjct: 64 WYFKCCGQIADQCCFRLQDWV 84

>ZK1037.6 [Full Sequence] [AceBrowser] CE16758 (HINXTON)  
Length = 491

Minus Strand HSPs:

Score = 52 (18.3 bits), Expect = 8.3, P = 1.0  
Identities = 11/22 (50%), Positives = 15/22 (68%), Frame = -2

Query: 105 FENIRNVIAEWIIDSCQLREDC 40  
+EN +N IA + SCQ+ HDC  
Sbjct: 244 YENTKN-IASFPQSISCQIMREDC 264

Parameters:

P=4  
warnings  
B=100  
filter=seg  
V=100  
C=1 (Standard genetic code)

ctxfactor=5.39

E=10

Query	Frame	MatID	Matrix name	----- Lambda	As Used K	----- H	----- Computed Lambda	K	----- H
Std.	0		BLOSUM62				0.318	0.135	0.401
+3	0		BLOSUM62	0.318	0.135	0.401	0.341	0.158	0.521
			q=9 r=2	0.244	0.0300	0.180			
+2	0		BLOSUM62	0.318	0.135	0.401	0.328	0.132	0.393
			q=9 r=2	0.244	0.0300	0.180			
+1	0		BLOSUM62	0.318	0.135	0.401	0.350	0.153	0.537
			q=9 r=2	0.244	0.0300	0.180			
-1	0		BLOSUM62	0.318	0.135	0.401	0.339	0.154	0.537
			q=9 r=2	0.244	0.0300	0.180			
-2	0		BLOSUM62	0.318	0.135	0.401	0.345	0.149	0.533
			q=9 r=2	0.244	0.0300	0.180			
-3	0		BLOSUM62	0.318	0.135	0.401	0.381	0.170	0.592
			q=9 r=2	0.244	0.0300	0.180			

Query

Frame	MatID	Length	Eff.Length	E	S	W	T	X	K2	S2
+3	0	78	73	10.	51	3	12	22	0.095	31
							27		0.12	31

+2	0	79	79	10. 53 3	12 22	0.11 31
					27	0.11 32
+1	0	79	79	10. 53 3	12 22	0.11 31
					27	0.11 32
-1	0	79	52	10. 45 3	12 22	0.11 29
					26	0.084 29
-2	0	79	65	10. 47 3	12 22	0.11 30
					27	0.092 31
-3	0	78	78	10. 53 3	12 22	0.10 31
					27	0.11 32

## Statistics:

Database: /data/blastdb/wormpub/wormpep\_current

Title: wormpub/wormpep\_current

Release date: unknown

Posted date: 12:07 PM BST Apr 24, 2001

Format: BLAST

# of letters in database: 8,675,472

# of sequences in database: 19,835

# of database sequences satisfying E: 33

No. of states in DFA: 581 (114 KB)

Total size of DFA: 253 KB (256 KB)

Time to generate neighborhood: 0.00u 0.01s 0.01t Elapsed: 00:00:00

No. of threads or processors used: 4

Search cpu time: 5.55u 0.65s 6.20t Elapsed: 00:00:17

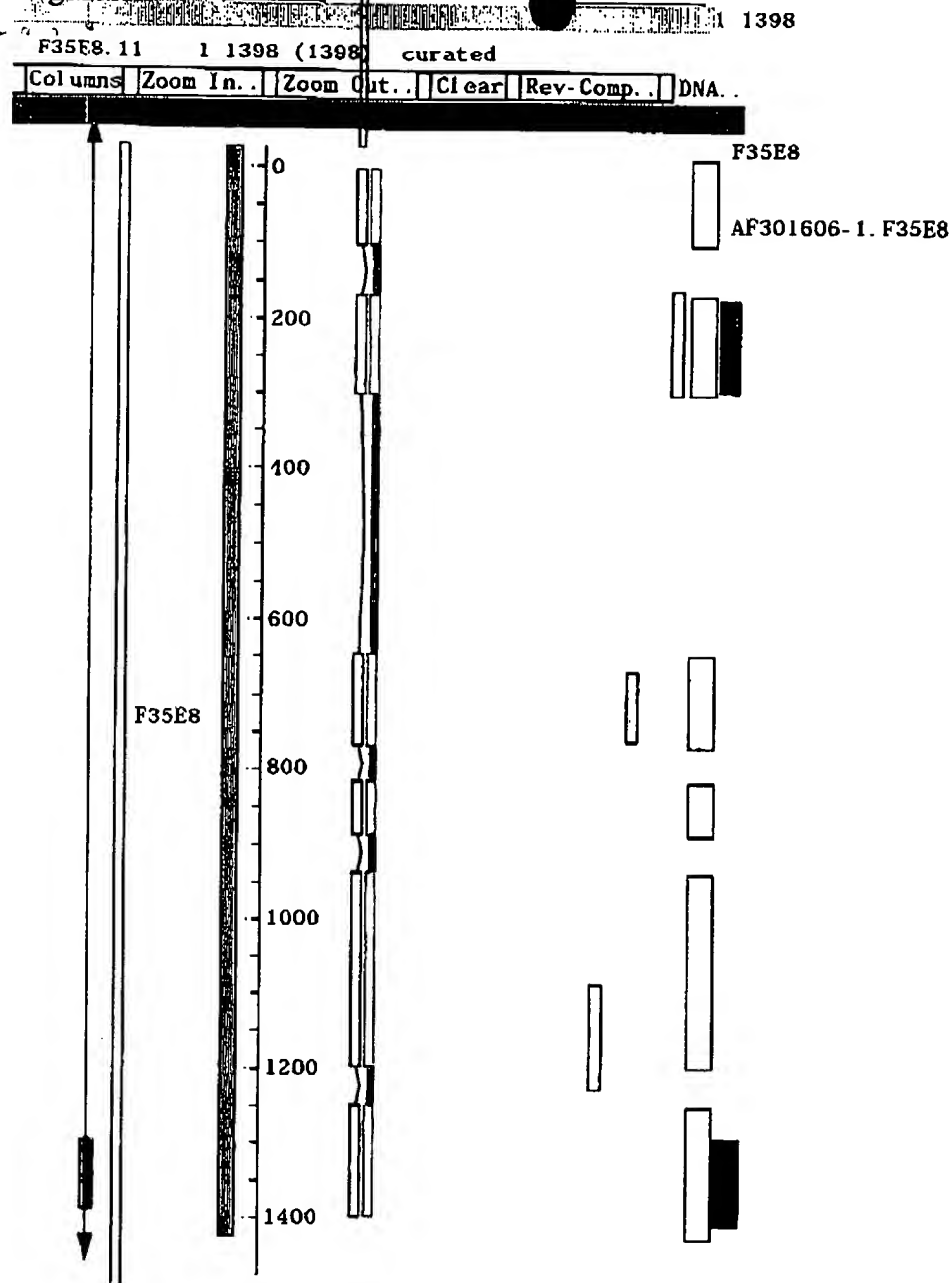
Total cpu time: 5.66u 0.86s 6.53t Elapsed: 00:00:24

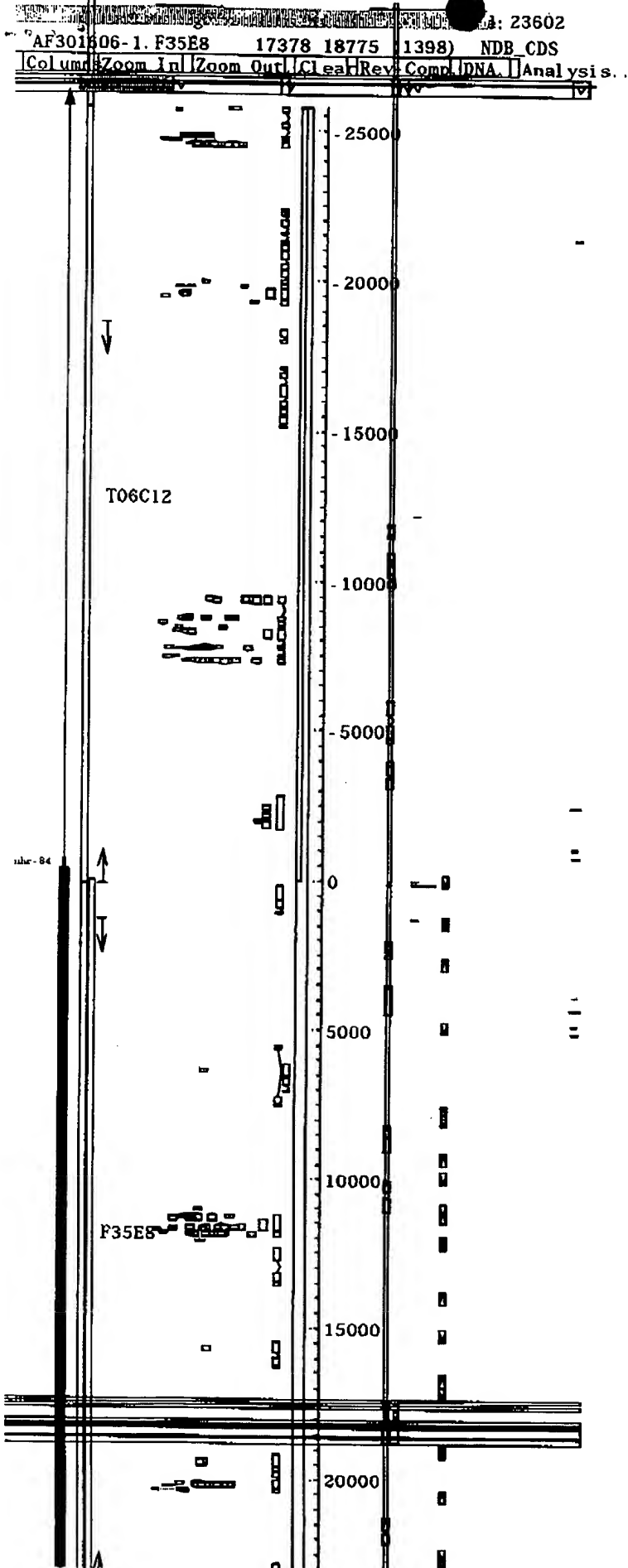
Start: Thu May 17 17:05:07 2001 End: Thu May 17 17:05:31 2001

http last modified Mon Apr 23 17:35:41 2001

[webmaster@sanger.ac.uk](mailto:webmaster@sanger.ac.uk)

Figure 6





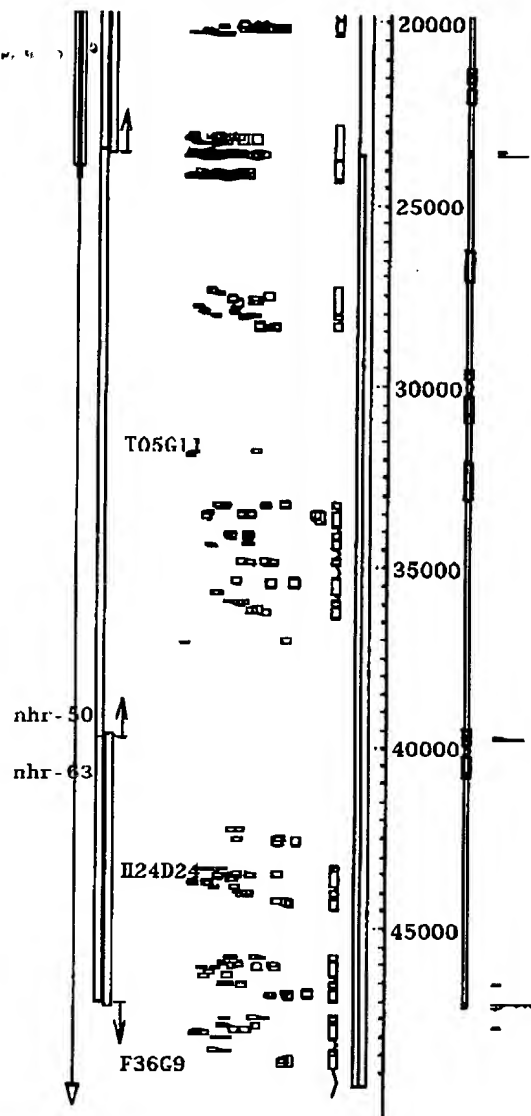


Figure 7

>F35E8.11 Glutathione S-transferases.

atgttggattcatgtttgattattactgctgcgctgttttggagccgctgt  
catttacttgaaaaatttcttactgttccttagcattaaaccaaaccctg  
atattcacaaaaaagactacaaaaaggatgtagtctatctgtatcagatg  
aagagactcaagaactgtccgaacttgcccccttctgcatgaaaatcga  
gattctttgtagaatcttcaagattccttacgagattatcacatgcacct  
ctgaacgctctcgggaatggattggtoctttogttgaactcaatggagag  
cacattgctgattctgatcttatcgaaatgcgcttgagatcacattttaa  
aattcgcgcgttccaactgagctggaaactcaatctgttgctctaagca  
agtttgcagatcaccatttggttcttcgtacttatacgattt.aaaattgct  
gtcgacgaattctacaaaaccattattgaaataatcgggtctcccaacctt  
cctgaatttcttctcatgccccctttgaaggctataatcgggaaaaatg  
tctacaacaaatgtcagggagccattggagattttgaattgagtgagctc  
gacgagattcttcacagagatttgcgaaatcgtagagaacaccttggccaa  
gaaaaagtttcttttcggggagggaatcacggcggcggatgcaacagtct  
tctctcaattggcaactgtctattatccattccgcaatcacatttcggat  
gttctcgaaaaggacttcccaaagttattggagtactgtgaaagagttcg  
tcatgaagtttacccaaaggactttactatgtga

Figure 8

>F35E8.11 Glutathione S-transferases.

MLDSCLIIITAALFGAAVIYLNFFTVPSIKPKPDIIHKKDYKKDVVYLYQM  
KRLKNCNLSPPFCMKIEILCRIFKIPYEIITCTSERSRNLVPPFVELNGE  
HIADSDLIEMRLRSHFKIPSLPTELETQSVALSKFADHHLFFVLIRFKIA  
VDEFYKTIIEIIGLPTFLNFLMPLLKAIIGKNVYNKCQGAICDFELSEL  
DEILHRDLRIVENTLAKKKFLFGEEITAADATVFSQLATVYYPPFRNHISD  
VLEKDFPKLLEYCERVRHEVYPKDFTM\*